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Location/Qualifiers
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AU143295.1 GI:11004816
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99.4%;
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Fax: 81-438-52-3952
                                                                        Matches 331; Conservative
                                Query Match \
Best Local Similarity
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Email: genomics6hr1.co.jp
HRI human cDNA project; 5' - & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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/note="vector: pMm18SFT3"
/note="vector: pMm18SFT3"
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Contact: Takao Isogai
Genomics Laboratory
Hellix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
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                                                                            Score 335.8; DB 1 Pred. No. 3.8e-31;
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188
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Best Local Similarity 99.4%;
Matches 337; Conservative
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TITLE JOURNAL

AUTHORS

REFERENCE

source

FEATURES

BASE COUNT

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AU143295 Y79AA1 Homo sapiens cDNA clone Y79AA1001699 5', mRNA
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Bukaryota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 739)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genomicsthri.co.jp
HRI human ChNA project; 5'-& 3'-end one pass sequencing: Helix
Research Institute; CDNA lbrary construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
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  Length 741;
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                                                Indels
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Contact: Takao Isogai
Genomics Laboratora Institute
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Score 329.8; DB 9;
Pred. No. 2.4e-30;
0; Mismatches 2;
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/note="Vector: pME18SEL3"
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801 aaaaggogogoggaaggggtootgocaccgocacttggoctgoctcogtoccgcogcg 860

Conservative

Matches 329;

Length 819;

DB 9;

Score 328.2; DB 9 Pred. No. 3,5e-30;

27.68; 99.18;

Ouery Match Best Local Similarity

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Mismatches

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Matches 330; Conservative

Length 739;

DB 9;

27.68; 99.18;

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                     801 aaaaggegegeggaagggteetgeeacegegeeattggeetgeeteegteeegegeg 860
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                                                                                                                                                      Email: genomics@hri.co.jp
HRI human CDNA project; 5.- & 3'-end one pass sequencing: Helix
Wirology, Institute of Medical Science, University of Tokyo, and
Location/Qualifiers
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Tel: 81-438-52-3951
Score 328.2; DB 9
Pred. No. 3.7e-30;
0; Mismatches 3
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/cell_line="Y79"
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/organism="Homo sapiens"
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AU143180.1 GI:11004701
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
  Matches 330; Conservative
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243 c 2
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Email: qenomics@hri
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/Lissue_type="placenta"
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AL545940 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODI023YK20 5
AL545940.1 GI:12878592
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                 801 aaaaggogogoggaaggggtoctgocacogogocacttggoctcogtocogogog
                                                Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - France
Email: Segref@genoscope.cns.fr, Web : www.genoscope.cns.fr,
Location/Qualifiers
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98.8%; Pred. No. 4e-30;
tive 1; Mismatches 3;
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AGENCOURT_6456956 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5576962
BMACOURT_6456956 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5576962 Clone=Index 1.255/6962"

/clone=Index NIH_MGC_92"

/clone_Index Espea"=embryonal carcinoma, cell line"
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/note="organ: testis; Vector: pcMV-sport6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 2:5 kb. Library enriched for full-length clones and constructed by Life Technologies.
full-length clones and constructed by Life Technologies.
a 323 c 264 g 204 t Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 985) Email: ogapbe-remail.nih.gov
Tissue Procurement: ATCC
CDN Library Preparation: Life Technologies, Inc.
CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
R.G.E. Consortium/LLNL at:
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R.G.E. Consortium/LLNL at:
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Location/Conslitiers
Location/Conslitiers 1041 catcctccgctgcggcgtcaggaaggacggacgcacgggcaccgggcaccctgtcggtatt 1100 NIH-MGC http://mgc.nci.nih.gov/. National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. 980 180 241 CATCCTCCGCTGCGGCGTCAGGAAGGACGACCGCACGGGACCCGGCACCCTGTCGTTT 300 9 121 CGCCATGCCTGTGGCCGGCTCGGAGCTGCCGCGCCGCCGCCCTTGCCCCCCGCCGCAAGAA coacttggcctgcctccgtcccgccgccacttcgcctgcctccgtccccgccgccgccg 921 egocatgeetgtggeeggeteggagetgeeggeeeggeeeftgeeeegeeggaeagga 26.6%; Score 315.8; DB 10; Length 985; 97.9%; Pred. No. 9.2e-29; Live 0; Mismatches 7; Indels 0; 1101 cggcatgcaggcgcgctacagcctgagaggtga 1133 10 CGCCATGCAGGGGGGCGCTACAGCCTGAGAGATGA 333 /organism="Homo sapiens" /db_xref="taxon:9606" BM466216.1 GI:18515258 Best Local Similarity 97.9 Matches 320; Conservative .985 Similarity Homo sapiens 194 BM466216 numan. Query Match BASE COUNT ORIGIN ORGANISM DEFINITION REFERENCE AUTHORS TITLE JOURNAL COMMENT ACCESSION VERSION KEYWORDS 861 FEATURES BM466216 qq q 셤 q qq δ ğ δ a δ Q

Technologies. Contact: Fend Liang Life Technologies, a division of invitrogen 9800 Medical Center Drive Rockvill Maryland 20850, USA Fex: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fullength.invitrogen.com a others AL541351 AL7_FL002_PL1 Homo sapiens cDNA clone CSODE0067A08 5 prink /note="Organ: placenta; Vector: pCNVSPORT 6; 1st strand cons was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Eukaryoja; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1047 cogotigoggostcaggaaggacgacogcacoggcaccoggcacctgtcggtattcggcat 1106 987 egecgageegegteegeegeaeggggagetgeagtacetggggeagateeaacateet 1046 0; Gaps 927 gcctgtggccggctccgagctgccgcgccgcgcccccgccgcacaggagcggga 986 Genoscope - Centre National de Sequencage Genoscope - Centre Cedex - France BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr. Location/Qualifiers Length 668; Indels Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope Score 310.4; DB 9; Pred. No. 4.9e-28; 1; Mismatches 2; /clone_lib="LTI_FL002_PL1" /lab_host="DH10B" /organism="Homo sapiens" /db_xref="taxon:9606" /clone="CS0DE006YA08" gcaggcgctacagcctgagaggtga 1133 AL541351.1 GI:12872339 26.1%; (bases 1 to 668) Conservative mRNA sequence. Similarity Homo sapiens AL54135. human. Matches 311; Query Match Best Local S. source BASE COUNT ORGANISM DEFINITION TITLE JOURNAL COMMENT REFERENCE AUTHORS 1107 ACCESSION VERSION KEYWORDS FEATURES AL541351 ORIGIN SOURCE LOCUS δλ g δŽ g ŏ qq ŏ q õ 음

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BM473957 AGENCOURT

AL515911 AL515911 AL551817 AL551817

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BF685317 602141676

AL548721 AL548721 AL547612 AL547612

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BM456638 1060 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6408748 NIH_MGC_85 Homo sapiens CDNA.clone lMAGE:5496315
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Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1060)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Finsue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
CLNA Gistribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
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High quality sequence stop: 530.
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Contact: Robert Strausberg, Ph.D.
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HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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AU128726.1 GI:10989080
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Fax: 81-438-52-3952
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 711)
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                                                     955 eggeeectgeeecegeegeacaggagegggaeggeegageegeegeegeegeaeggggag 1014
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="retinoblastoma"
/cell_line="Y79"
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208 q 139
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/db_xref="taxon:9606"
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/clone_lib="Y79AA1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genomics@hri.co.jp
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                                                                                                                                                                                                                                                         AU142980.1 GI:11004501
                                                                                                                                                                                                                                                                                                                                                                                              HRI human cDNA project
                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 81-438-52-3951
Fax: 81-438-52-3952
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Matches 296; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
1075 acgggcaccggcaccctgtcggtattcggcatgcaggcgcgctacagcctgagaggtga 1133
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                                                                                                                                                                        AU128726 AU2RP2 Homo sapiens CDNA clone NT2RP2004045 5', mRNA
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone="NIZRE2104045"
/clone_lib="NTZRE2"
/cell_type="teratocarcinoma"
/cell_line="NT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helix Research Institute.
Location/Qualifiers
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BIS97722 905 bp mRNA linear EST 07-SEP-2001 603248376F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5300034 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
GDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carnino: (RIKEN)
GDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="organ: brain; Vector: pBluescriptR (modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc. clone distribution: MGC clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://imaqe.llnl.gov column: 19
Plate: LLAM11759 row: h column: 19
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98.3%; Pred. No. 3.2e-25;
Live 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Location/Qualifiers
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/clone="IMAGE:5300034"
1111 gegegetaeageetgagaggtga 1133
                     323 GCGCGCTACAGCCTGAGATGA 345
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Matches 289; Conservative
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                                                                    BE794349 529 bp mRNA linear EST 20-SEP-2000 601589526F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3943615 5',
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                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 529)
NIH-WGC http://mgc.nci.nih.gov/.
Nat.bonal Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="WGC3"
/lab_host="DH10B (phage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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/clone="IMAGE:3943615"
                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
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                                                                                                                   mRNA sequence.
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AUTHORS
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KEYWORDS
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Search completed: July 26, 2002, 15:13:23 Job time: 26887 sec

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Genomic sequence #
Human genomic DNA

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Assaying method, useful for prognosis and diagnosis of disease, comprises contacting sample with a mutant analyte-binding enzyme and detecting binding -
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                  5605 T; 0 other;
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                                              Score 1163.8; DB 2.
Pred. No. 8.6e-192;
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The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atheroscierosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as POR primars and probes. The polynucleotide sequences can also be used useful in gene therapy. Assign the invention are also polynucleotide sequences of the invention are also polynucleotide sequences of the invention which are differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development
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Ctgcccccogcogcacaggagcggacgccgagccgagtccgccgcacgggggagctgcag
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DB 24; 4;

Score 287.2; DB 24 Pred, No. 5.8e-41; 0; Mismatches 4;

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Isolated polypeptide for treating, preventing and/or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.

Example 2; SEQ ID NO 3534; 781pp + Sequence Listing; English.

The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)aponists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune gastrointestinal tract, liver, lung, or urogenital; (b) immune control and thyroiditis, diabetes mellitus, crohn's disease, continued thyroiditis, diabetes mellitus, cohn's disease, contitue sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and it, infectious diseases such as viral, bacterial, fungal and Note: The sequence data for this patent did not form part of parasitic infections.

Sequence 9519 BP; 2702 A; 1682 C; 1664 G; 3471 T; 0 other;

from WIPO at ftp.wipo.int/pub/published_pct_sequences.

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specification, but was obtained in electronic format directly

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Length 9519;
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  DB 22;
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            4.1e-27
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  Score 206.8;
Pred. No. 4.1
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Human; reproductive system related antigen; reproductive system disorder;
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quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AASS4197-AASS454 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                      Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                                                       Sequence 1539 BP; 396 A; 37.9 C; 347 G; 417 I; 0 other;
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20-OCT - 2000;
08-NOV - 2000; 05-JAN-2001;

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM; Barash SC, Rosen CA,

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 28083; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic

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Ruben SM;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

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Disclosure, SEQ ID NO 21686; 3071pp + Sequence Listing; English.

XX
AX54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
Cx amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
c activity, and can be used in gene therapy and vaccine production. (I)
Cx cample, they may be used in gene therapy and vaccine production. (I)
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Cx cample, they may be used to tract disorders associated with decreased
Cx cample, they may be used to tract disorders associated with decreased
Cx cample, they may be used to produce the secreted (I) by inserting
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Cx concers and cancer metastases of haematopoietic antigen genomic
Cx represent sequences used in the exemplification of the present invention.

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Sequences 17449 BP; 11842 A; 7890 C; 7531 G; 10186 T; 0 other;

4; 23253 AAAAAAGAAGTGTAATAAAGCTTCATAGATTTATCATCCAGACTAAATTATCAGTATTT 23194 22956 GTGATACGCCCCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCATGAGGCACTGCGCCC 22897 23193 ACCAMGITITCITITITITITAGAGAGICICGCICIGICGCCCAGGCIAGAGIGCAG 23134 23133 TGGCATGATCTCGGCTCACTGCAAGCTCCACTCCCAGGTTCAAGCGATTCTCCTGCCTC 23074 61 aaa----aagaccgccagggctcaaacaaaaaacctcggaaaagccctggcggtctttt 116 117 tittittittittittittitgggacagtettgetetgtegeceaggetggagtacaa 176 tggteggatettggeteaetgeaacetetgeeteecaggtteaageaattettetgeete 236 tttagtagagacggggtttcaccatgttgtccaggctggtctngaactcctgacctcag 337 grgatecaccegecteggecececaaagtactaggattacaggegtgagecacegegtee 397 26; Gaps Score 204.2; DB 22; Length 37449; 80; Indels Pred. No. 1.2e-26; 0; Mismatches 80 17.2%; 74.9%; Query Match 17.2 Best Local Similarity 74.9 Matches 317; Conservative 278 338 177 g g G 음 셤 쉼 셤 ğ δ δ δ ŏ 임 QΥ ă

AAK68202 standard; DNA; 56743 BP.

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AAK81760
            RESULT
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                                                                                                                                                                                                                                                                example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, addingnose and treat immune/lammatopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703
                                                                                                                                                                                                                                                                                                                                                                                                                                   represent sequences used in the exemplification of the present invention.
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Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36572.
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AAK81760 standard; DNA; 56743 BP.
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                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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                                                                                                                           2249 aagtatccttttaataacttggaataaag 2277
                                                                                          402 ccctggcggtttttaatcaagtagaaag
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and artifatory and can be used in game therapy and vaccine production. (I) activity, and can be used in gene therapy and vaccine production. (I) cartifaty, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynuclectides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynuclectides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic artifact general promits cancers muther present invention. AAKS4942 to AAKS4950 and AAMS2169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, actuating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 20117; 3071pp + Sequence Listing; English.
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                                                                                            2000US-0249297.
2000US-0249299.
2000US-0249300.
2000US-0250160.
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Query Match 17.1%; Score 202.6; DB 22; Length 22916;
Best Local Similarity 81.9%; Pred. No. 2.2e-26;
Matches 245; Conservative 0; Mismatches 51; Indels 3; Gaps 16 tttttttttttttttttttttgggacagtcttgctctgtcgcccaggctggagtaca 175

296 ttcaccatgttgtccaggctggtctngaactcctgacctcaggtgatccacccgcctcgg 355

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Nucleic acids encoding 3224 human nervous system antigen polypeptides,
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or amelicating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful. The nucleic acids, proteins, antibodies and (ant)agonists are useful. In the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; of himmune disorders e.g. Addison's disease, allergies, autoimmune themolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, theumatoid arthritis and ulcerative of the additional and paragine infectious diseases such as myocardial ischaemias; child protein and parasitic infectious diseases such as viral, bacterial, fungal material and parasitic infections diseases and parasitic fungal
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diagnosing and/or treating nervous system
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Database

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HUMIS 1186 bp DNA linear PRI 06-NOV-2001
Homo sapiens gene for thymidylate synthase, exon 1, partial cds.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human thymidylate synthase gene: isolation of phage clones which cover a functionally active gene and structural analysis of the region upstream from the translation initiation codon 3. Biochem. 106 (4), 575-583 (1989)
                                                                           AX330682 Sequence
AX330906 Sequence
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Takeishi, K., Kaneda, S., Ayusawa, D., Shimizu, K., Gotoh, O. and
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Sequence

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University of Shizuoka School of Food and Nutritional Sciences 395 Yada

Takeishi

Description

Query Score Match Length DB

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Result

Db 1097 TACCTGGGGCAGATCCAACATCCTCCGGTGGGGGTCAGGAAGGA	RESULT 3 AX050451 LOCUS LOCUS DEFINITION Sequence 11 from Patent W00071754. ACCESSION AX050451 VERSION KEYWORDS	SOURCE Numan. ORGANISM Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 18596) AUTHORS Johnson, W.G. and Stenroos, E.S. TILLE Methods for diagnosing; preventing, and treating developmental	ders due to a combination of generic and envisorments of E: Wo 0007754-A 11 30-NOV-2000; rsity of Medicine and Dentistry of New Jersey (US) Location/Qualifiers Lorganism="Homo sapiens" /db_xref="taxon:9606"	BASE COUNT 4521 a 3991 c 4479 g 5605 t ORIGIN Query Match Bast Local Similarity 99.1%; Pred. No. 3e-191; Bast Local Sinches 1176: Conservative 0: Mismatches 10; Indels 1; Gaps 1;	ogccactgcactccagcctgggtgagagcgagactctgtctcaaaaaaaa			Oy 241 toccaagtagccaccagctaatttttgtanttttagtagaacggggtttcac 300		421 agtagaaagctgcattataccacttgcttcngttgcnttcagtgagaacgaagaatgg 421 agtagaaagctgcattataccacttgcttcngttgcnttcagtgagaacgaagaatgg 498 AGTAGAAAAGCTGCATTGCTTGGGTTGC-TTCAGTGAAAAGCAAAGAAATGG	$Q_{ m Y}$ 481 aaatgcaaatAncttattagttgtaggaaacagatctcaaacagcagttttgtngacaag 540
Best Local Similarity 99.1%; Pred. No. 3e-191; Matches 1176; Conservative 0; Mismatches 10; Indels 1; Gaps 1; Qy 1 gatcgccactgcactccagcctgggtgagagagcgagactctgtctcaaaaaaaa	121 tttttttttttttttttgggacagtcttgtctgtcgcccaggctggagtacaatggt	241 teccaagtagecaccacgeccagtaatttttgtanttttagtagagaggggttteac	GTGATCCACCCGC ggcgccctggcggf 		aacgtgggaactgtgctgcttggcttagagaaggcgcggtcc 		721 ccctggcgcacgctctctagagcggggccgcgcgcgcgcg	QY 781 gag-gaggacagggaaaaggggcggggaagggtcctgcaccgccacttgg 840 DD 857 gadcgcggcacagaaaaggggcccaggaaagggcccacctaggcccacttgcacgcac	scccccca gagetgeeg 	Qy 961 Ctgcccccgccgcacaggagcggagcgggacgcgcgcgccgc	

18 AGIAGAAAAGCTGCATTATACCACTTGCTTCGGTTGC-TTCAGTGAGAACGAAGAAATGG 556	661 agactctcagotgtggctcgttctgtgccacacccgtggctcctgggtttc 7 111111111111111111111111111111111111		RESULT 6 AX335755 AX335755 AX335755 AX335755 ACCESSION AX335756 ACCESSION AX335756 ACCESSION AX335756.1 G1:18126474 AX335755.1 G1:18126474 AX335755.1 G1:18126474 AX335755.1 G1:18126474 AX335756.1 G1:18126474 AX335756.1 G1:18126474 AX335756.1 G1:18126474 AX335756.1 G1:18126474 AX335756.1 G1:18126474 AX335756.1 G1:18126474 AMMANIAL AND A PLEADAR CALARTHINI; HOMINIGAE; HOMO. REFERENCE I (sites) AUTHORS YOUNG P.E. Augustus, M. Carter, K.C., Ebner, R. Endress, G., HORTIGAD, S., Soppet, D.R. and Weaver, Z. HORTIGAD, A. S. Soppet, D.R. and Weaver, Z. HORTIGAD, A. S. Soppet, D.R. and Weaver, Z. HORTIGAD, A. Carter, M. O194629-A 6264 13-DEC-2001; Avalon Pharmaceuticals (US) LOCATION/QUALIFIERS 1. 18556 Avalon Axafier Taxon:9606"
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FEATURES Location/Qualifiers source 11186 //organism="synthetic construct" //organism="synthetic construct" //db_xref="taxon:32630" //db_xref="chamically treated genomic DNA (Homo sapiens)" BASE COUNT 229 a 98 c 386 g 473 t ORIGIN	Query Match 64.7%; Score 767.4; DB 6; Length 1186; Best Local Similarity 78.4%; Pred. No. 6.2e-123; Matches 926; Conservative 0; Mismatches 254; Indels 1; Gaps	QY 2 atcgcgccactgcactccagcctgggtgagagcgagactctgtctcaaaaaaaa	OY 62 aaaagaccgccagggctcaaacaaaaacctcggaaaagccctggcggtctttttttt	OY 122 ttttttttttttttttgggacagtcttgctctgtcgcccaggctggagtacaatggtc 181	Oy 182 ggatettggeteaetgeaaectetgeeteeagtteaageaattettetgeeteageet 241	Qy 242 cccaagtagccaccacgcccagctaattttgtanttttagtagagacgggggtttcacc 301	Oy 302 atgitgiccaggctggtctngaactcctgacctcaggtgatccaccgcctcggccccc 361	OY 362 aaagtactaggattacaggcgtgagccaccgcgtccagcgccctggcggtttttaatcaa 421	QY 422 gtagaaagctgcattataccacttgcttcngttgcnttcagtgagaacgaagaaatgga 481	Qy 482 aatgcaaatAnottattagttgtaggaaacagatctcaaacagcagttttgtngacaaga 541	OY 542 ccgcaggaaacgtgggaactgtgctggcttagagaagggggggg	OY 602 teccaaagggggagtettecengceacegeactgentecaggttecegggtntecta 661	OY 662 agactotcagctgtgggctccgttctgtgccacacccgtggtcctgcgtttcc 721	OY 722 ccctgggggcacgctctctagagcgggggccgcggggacccgcggggagggggggg	OY 782 agoggggacggggaaaaggcgcgggaaaggggtcctgccaccgcgccacttggc 841	OY 842 ctgcctccgccgccgccacttggcctgcctccgtcccgccgcgcgcacttcgcctgc 901
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Qy Db

QY Db

QY DP

Q Q

QY Db QΣ Dp

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RESULT 9
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                                                                                Gaps
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Location/Qualifiers
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                                                            Query Match
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LOCUS
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/translation="mpVMGSELPRRPLPPAAOERDAEPRPPHGELQYLGQIQHILRCG
VRKDDRTGTGTLSVFGWQARYSLRDEFPLLTTRRVFWKGYLEELLWFTKGSTRAKELS
SKGYKIWDANGSRDFLDSLGFSTREEGDLGPYVGPQWRHEACERTRMESDYSGQVDQ
LQRVIDTIKTWDDRRIIMCAWNPRDLPLMALPPCHALCQFYVWSELSCQIYQRSGD
MGLGYPFWLASYSLLTYMALATTGLKFGDFTHTLGDAHLCQFYVWSELSCQIYQRSGP
MKLRILRKVEKIDDFRAEDFQIEGYNPFPIRMEMAV"
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Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Shiffman.D., Somogyl,R., Lawn,R., Sellhamer,J.J., Porter,G.J.,
Mikita,T. and Tai,J.
Genes expressed in foam cell differentiation
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1519. 1524
/note="pot. polyadenylation signal"
1536
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Pred. No. 4.3e-42;
0; Mismatches 2;
/note="pot. stem-loop structure"
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                                                                                                                                                                                          /protein_id="CAA26178.1"
/db_xref="G1:37479"
/db_xref="SWISS-PROT:P04818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="polyadenylation site" 369 c 378 t
                                                                                                    104. .106
/note="direct repeat 1"
106. .1047
/note="thymidylate synthase
                                                                        /note="inverted repeat A''"
104. .106
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Sequence 200 from Patent WO0177389.
                                              'note="direct repeat 1"
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                                                                                                                                                                           /codon_start=1
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Best Local Similarity 99.3%;
Matches 299; Conservative
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site:

nisc_mgc@nhgri.nih.gov/
Contact:
nisc_mgc@nhgri.nih.gov/
Shevchenko,Y., Wetherby,K.D., Beckstron-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,B.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiAL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: p Column: 19
Stries: IRAL Plate: 4 Row: p Column: 19
This clone was selected for inl1 length sequencing because it passed the following selection criteria: matched mRNA gi: 4507750.
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MGLQVPRNIASYALLIYWIAHITGLRQDPIHTIGDAHIYLNHIEPLKIQLQREPRPF
PKLRILARVEKIDDRAEDPQIEGYNPHPTIKMEMAV"
PKLRILARVEKIDDRAEDPQIEGYNPHPTIKMEMAV"
359 c 389 g 376 t
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SKGVKIWDANGSRDFLDSLGFSTREEGDLGPVYGFQWRHFGAEYRDMESDYSGQGVDQ
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/clone_lib="NIH_MGC_21"
/lab_host="DH10B-R"
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/protein_id="AAH02567.1"
/db_xref="G1:12803483"
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/organism="Homo sapiens"
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Search completed: July 26, 2002, 16:39:18 Job time: 24232 sec Appli Appli Appl Appl Appl Appl Appl

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Sequence 1, Application US/09089195

Sequence 1, Application US/09089195

Patent No. 6087489

GENERAL INFORMATION:

APPLICANT: Dean, Nicholas M.

TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDE MODULATION

TITLE OF INVENTION: OF HUMAN THYMIDYLATE SYNTHASE EXPRESSION

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESSS:

ADDRESSEE: Law Offices of Jane Massey Licata

STREET: 66 East Main Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Seno,T.

Nuclectide sequence of a functional cDNA
Nuclectin human thymidylate synthase
Nucleic Acids Res.
         US-08-483-533-18
US-09-283-471A-18
US-09-165-283-4
US-09-123-471A-4
US-09-123-471A-4
US-09-123-471A-4
US-09-123-33-38
US-09-283-471A-38
US-09-283-471A-38
US-09-283-471A-38
US-09-283-471A-38
US-09-283-471A-38
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US-08-999-733-1
US-09-043-303-5
US-07-945-283-1
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US-08-093-453B-1
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APPLICATION NUMBER: US/09/089,195
FILING DATE: herewith
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: ISPH-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 810-1454
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 base pairs
TYPE: NUCleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION: NAME: Jane Massey Licata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: Single TOPDLOGY: Unknown PUBLICATION INFORMATION: AUTHORS: AUTHORS: AUTHORS: AUTHORS: Shimizu, K. AUTHORS: Gotoh, O.
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
Marlton
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                               alignments)
Million cell updates/sec
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Sequence 17, Appl
Sequence 7, Appl
Sequence 7, Appli
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/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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4 US-09-20-371A-17

5 US-08-757-669A-17

6 US-09-265-315-7

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1 US-09-128-155-16

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Maximum Match 100%
Listing first 45 summaries
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APPLICANT: Nicholas, John
APPLICANT: Nicholas, John
APPLICANT: Reitz, Marvin
TITLE OF INVENTION: No. 6264958el Genes of Kap
TITLE OF INVENTION: No. 6264958el Genes of Kap
TITLE OF INVENTION: Associated Herpesvirus
TITLE OF INVENTION: No. 6264958el Genes of Kap
TITLE OF INVENTION: NO. 6264958el Genes of Kap
TITLE OF INVENTION: 1107.78372
CURRENT APPLICATION NUMBER: 1999-11-23
CURRENT FILING DATE: 1999-11-23
PRIOR FILING DATE: 1996-07-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: PCT US 97/12931
PRIOR FILING DATE: 1997-07-24
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Patent No. 6264958
GENERAL INFORMATION:
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LENGTH: 1014
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Score 387.4; DB 4;
Pred. No. 1.8e-93;
0; Mismatches 341;
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                                                                                                                                           Score 387.4; DB 4;
Pred. No. 1.1e-92;
0; Mismatches 341;
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
               17:
                                                           STRANDENESS: double
STRANDENESS: double
FOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-669A-17
                                                                                                                                            Query Match 25.2%;
Best Local Similarity 63.5%;
Matches 592; Conservative
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GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenaky, Roy A
APPLICANT: Roleman, James J
APPLICANT: Roleman, Isidore S
APPLICANT: Roleman, Isidore S
APPLICANT: Moore, Patrick S
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS SEQUENCES AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 45185-G-PCT-US
20183 TCIGTICTICCAIGGAAGAGITIACACCIGAIGAITITAGACIGGIGGACIACIGCCCG 20124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20963 GCTGAGACGCCCCACGAGGAACTTCAGTATCTCAGGCAGTTGAGGGAATTTGTGCCGT 20904
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Pred. No. 1.1e-92;
0; Mismatches 341; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA; CAPOSI's sarcoma-associated herpesvirus US-09-230-371A-17
                                                                                                            20123 CATCCTACCATTCGTATGGAAATGGCAGTATAG 20091
                                                               catccaactattaaaatggaaatggctgtttag 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: 05/09/230,371A CURRENT FILING DATE: 1999-11-17 PRIOR APPLICATION NUMBER: PCT/US97/13346 PRIOR FILING DATE: 1997-07-22
                                                                                                                                                                                                                                                                   ; Sequence 17, Application US/09230371A; Patent No. 6348586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.2%;
Best Local Similarity 63.5%;
Matches 592; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                RESULT 6
US-09-230-371A-17/c
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APPLICANT: Sun, Dongara
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

RELING DATE: March 9, 1999

PRICASSIFICATION: 435

PRICA APPLICATION: 435

PRICA APPLICATION: 435
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
                                                                                                                                                                                                                   E: Lyon & Lyon
633 West Fifth Street
Suite 4700
              Lee, Ving J.
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
Benton, Bret
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                Los Angeles
California
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90071-2066
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STREET: 63
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US-09-265-315-7
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STATE: CZ
COUNTRY:
                                                                         APPLICANT:
APPLICANT:
                APPLICANT:
APPLICANT:
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Pred. No. 1.7e-22;
6; Mismatches 194;
                OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
                                                                                                                                                      APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFERMATION:
                                                                             US/09/265,315
                                                                                                                                                                                                                                                                                                                                             240/247
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US-09-265-315-7/c
; Sequence 7, Application US/09265315
; Patent No. 6187541
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INPORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3479 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                     NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 24(
TELECOMMUNICATION:
                                                                             APPLICATION NUMBER: US/09/:
FILING DATE: March 9, 1999
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  IBM Compatible
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Matches 268; Conservative
                                                      CURRENT APPLICATION DATA:
                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-09-265-315-7
                                                                                                                   CLASSIFICATION:
                                                                                                FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.9%; Score 121.2; DB 4; Length 56.8%; Pred. No. 1.7e-22; tive 6; Mismatches 194; Indels
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32.427
TERFORMER 32.427
                                                                                                                                          REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                          TELEFAX: (213) 955-0440
TELERX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 34'9 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                           (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 268; Conservative
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Best Local Similarity
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REFERENCE/DOCKET NUMBER: 28097/32742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/483,533
07-MAR-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 37, Application US/08483533
Patent No. 6172047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
08/419,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07/861,233
      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                      TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-886
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                      LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-APR-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-92
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Illinois
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                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                70 ccacttogcctgcctccccccgcccgccgcgcgccatgcgtggccggctcggagctg 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 ccgcgcccggcccttgccccccgccgcacaggaggggacgccgagccgcgtccgccgcac 189
                                                                                                                                                                                                                                                                                                                                                                                           413 GCGCGCCTGCGCCTGCGACGCGCGGGGGGGGGGGCGCCGGGAGCCCCCCGGGACCCCC 472
                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases
                                                                                                                                                                                                                                                                        Query Match 3.2%; Score 48.6; DB 4; Length 503; Best Local Similarity 54.1%; Pred. No. 0.0012; Matches 99; Conservative 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 27373/32742A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/283,471A FILING DATE: 04-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 7, Application US/09283471A
; Patent No. 6340673
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/861,233
APPLICATION NUMBER: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08/483,533
                TELEFAX: 312/4/*
TELEFAX: 312/4/*
TELEFAX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 11-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRAL
STREET: 62.
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60606-6402
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70 ceacttogectgectcegteecegeeegeegegecatgectgtggeeggeteggagetg 129
                                                                                                                                                                                                                                                                                                                                       353 GGCCCTTCCGCCGCGCCTCCGCCTCCGCCTCGCGTCACCGCGGAGCACCTC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                     293 GGGCCCCCACCGCCGGCGTGGGCCCGGGGGGCGGGCTGACCCCTCCCACCCCCCTCG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                          130 ccgcgccggcccttgcccccgccgcacaggagcgggacgccgagccgcgtccgccgcac 189
                                                                                                                                                    10 gggaccacttggcctgoctccgtccgccgccgccacttggcctgcctccgtccgccgcg 69
Query Match 3.2%; Score 48.6; DB 4; Length 503; Best Local Similarity 54.1%; Pred. No. 0.0012; Matches 99; Conservative 0; Mismatches 84; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Roizman, Bernard
APPLICANT: Chou, Joany
TITLE OF INVENTION: Method for Treating Tumorigenic
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
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0;
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                                                                                                                                                                                                                                              ;
0
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TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANII-SENSE: NO

ORIGINAL SOURCE:

CREANISM: Herpes simplex virus

STRAIN: Herpes Simplex virus

FEAUTHE:

NAME/KEY: CDS

LOCATION: 1..702

US-08-458-568A-3
                                                                                                                                                                                                                                                                                                                                                                                                   gg 192
                                                                                                                                                                                                                                                                                                                                                                                                                              184 CG 183
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Search completed: July 26, 2002, 17:46:36 Job time: 12445 sec

thuse are the edited sugs to 657; all edits are

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APPLICANT: Stanton, Jr., Vincent P.
TITLE OF INVENTION: THYMIDINE SYNTHASE GENE SEQUENCE VARIANCES
TITLE OF INVENTION: HAVING UTILITY IN DETERMINING THE TREATMENT
FITLE OF INVENTION: OF DISEASE
FILE REFERENCE: 11926-015002
                                                                                                                                                                                                                   PRIOR PELLING JATES 2001.

PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/596,033
PRIOR APPLICATION NUMBER: 09/596,033
PRIOR FILING DATE: 2000-06-15
PRIOR PELLING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1999-07-19
PRIOR FILING DATE: 1998-07-10
SOFTWARE: FastSEQ IO NUMBER: 60/093,484
PRIOR FILING DATE: 1988-07-20
NUMBER OF SEQ ID NOS: 16
SEQ ID NO 650
SEQ ID NO 650
                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/963,333 CURRENT FILING DATE: 2001-09-24
Sequence 6, Application US/09963333 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1066
OTHER INFORMATION: n = t or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n = a or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 1136
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ggačajtettgetetgtegeceagetgggtacaatgjteggatettggeteattgetee ecaggtteaageaattettetgeeteageeteecaagtageeaceaegeecagetaattttgtantttt agtagaacgggggttttcaccatgttgtccaggctggtctngaactcctgacctcaggtgatccacccgc ciogócócocóaaagtactaggaitacaggogígagocacgogtocagogocotggoggtutttaatca agtagaaaagetgoattataccacttgettengttgentteagtgagaaagaaatggaaaatggaaat Anctiattagittgiaggaaacagatcicaaacagcagttitgingacaagaccgcaggaaaacgigggaa ctytyctycigittägagaayýcycygtcyacóayácyyttccóaaayýgcycaytécttccóngécac cycactycntecayyttcccyyytntcctaayactctcayctytyyccctyyyetcoyttctytycoc accogtogotectogogitticeccetogococacoetetetagaocogogocogeogeogacecogocogagea ggaagagggaggaggaggacggccgcgggaaaaaggcgcgcgcgggaagggggtcctgccacgcgcacttgg cetgecteogice egecacitage et go et ce de care de carete de consecuente de consecuence de consecuencies de consecuencia de cons cegecegeegegeratgeetgtggeeggeteggagetgeegegeeggeeeftgeeecegeeggaagga gegggaegecgagecgegtecgecgeaeggggagetgeactggagtaeetggggeagatecaaeacatectecge tgeggegteaggaaggaeggeeggeeggggeaecgggeaeeetgteggtatteggeatgeaggegggegetaea Sequence 7, Application US/09963333
GENERAL INFORMATION:
APPLICANT: Stanton, Jr., Vincent P.
TITLE OF INVENTION: THYMIDINE SYNTHASE GENE SEQUENCE VARIANCES
TITLE OF INVENTION: BAVING UTILITY IN DETERMINING THE TREATMENT
TITLE OF INVENTION: OF DISEASE
FILE REFERENCE: 11926-015002 OTHER INFORMATION: nucleotide in position 458 is c, or absent PRIOR FILING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 09/596,033
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 09/357,743
PRIOR APPLICATION NUMBER: 09/357,024
PRIOR APPLICATION NUMBER: 00/357,024
PRIOR APPLICATION NUMBER: 00/937,484
PRIOR FILING DATE: 1998-07-19
NUMBER OF SEQ ID NOS: 16
SOFWWARE: FASTSEQ for Windows Version 4.0 CURRENT APPLICATION NUMBER: US/09/963,333 CURRENT FILING DATE: 2001-09-24 PRIOR APPLICATION NUMBER: 09/658,659 OTHER INFORMATION: n = c or a NAME/KEY: misc_feature LOCATION: 276, 321, 534, 656OTHER INFORMATION: n = c or OTHER INFORMATION: n = a NAME/KEY: misc_feature LOCATION: 492, 625 NAME/KEY: misc_feature LOCATION: 452, 640 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature LOCATION: 458 LENGTH: 1187

gócagttetatýtýgtgaacagtgagctýtcctgccagctgtaccagagatcgygagacatgygcttogg tytycrittcaacatcgocagttacgcctgctcacqttacagtgttggcacatcacagggcctgaagcca gytgactttatacacactttgygagttgcacatatttactgaatcacatcgagccatgaaaattcagc tcagogagaacocagacctttccaaagctcaggattcttcgaaaagttcgagaaaattgatcaca

gctttcaaaggagctCgaaggatattgtcagtctttaggggttgggctggatgccgaggtaaaagttctt tttgotctaaaaagaaGaaggaactaggtcaaaaatctgtccgtgacctatcagttattaatttttaagga tgttgccactggcaaatgtaactgtgccagttctttccataataaaaggctttgagttaactcactgagg tatgtgcatttcaatcccacgtacttataaagaaggttggtgaatttcacaagctatttttggaatattt

agctgaagactttcagattgaagggtacaatccgcatccaactattaaaatggaaatggctgtttaggg

ttagaatattittaagaattioacaagotatioooloaaatoigagggagotgagtaacaccatogateat gaigtagagigiggitatgaactitaAagitgitittataigitgotataaaaagaagigitotogol

agaatcaicatgigogottggaatocaagagaicttoctcigatggogotgoctocatgocatgoototot

toggcatgcaggcgcctacagcctgagagatgaattccctctgctgacaaccaaacgtgtgttctggaa

cagateceaacacatectecgetgeggegteaggaaggaeggaeegeaegggeaeeggeaeeetgteggta

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alignments)
Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 gggggggggggaccacttg.....ataataaagaagtgttctgc 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     M.GENESGY_032802;*

M.GENESGY_032802;*

2. (SIDSI/Gggdata/geneseq_genesequ-embl/NA1981.DAT:*

3. (SIDSI/Gggdata/geneseq_genesequ-embl/NA1981.DAT:*

3. (SIDSI/gggdata/geneseq_genesequ-embl/NA1983.DAT:*

4. (SIDSI/gggdata/geneseq_genesequ-embl/NA1984.DAT:*

5. (SIDSI/gggdata/geneseq_genesequ-embl/NA1984.DAT:*

6. (SIDSI/gggdata/geneseq_genesequ-embl/NA1986.DAT:*

7. (SIDSI/gggdata/geneseq_genesequ-embl/NA1986.DAT:*

8. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

9. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

10. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

11. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

12. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

13. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

14. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

15. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

16. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

17. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

18. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

19. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

20. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

21. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

22. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

23. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

24. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

25. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

26. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*

27. (SIDSI/gggdata/geneseq_genesequ-embl/NA1980.DAT:*
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                                                                                                                                                                                                                     July 26, 2002, 14:31:46; Search time 406.4 Seconds (without alignments) 6489.125 Million cell u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3472872
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1736436 segs, 858457221 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                      OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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1536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Human DNA sequence	DNA encoding novel	Thymidylate syntha	Human thymidylate	Human thymidylate	Nucleotide sequenc	Nucleotide sequenc	Macaca mulatta rha	Human herpesvirus
A	- 74	AAS84960	AAF31109	AAC91215	AAX24270	AAH74201	AAH74202	AAC64754	AAV10240
DB	24	23	22	22	20	22	22	21	13
% Query re Match Length DB I	3298	1539	18596	18596	266	124884	125157	26.3 133719	1014
% Query Score Match	97.3	83.4	39.9	39.6	32.6	26.6	26.6	26.3	25.2
Score	1494.8	1281.4	613.2	613.2	501.2	408	408	404.6	387.4
Result No.	~	7 U	m	4	5	9	7	œ ن	9

ALIGNMENTS

BP.

AAS94945 standard; DNA; 3298

/ AAS94945 ID AAS94

RESULT

AAS94945;

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Mikita T;
                                       Human DNA sequence #200 expressed during foam cell differentiation.
                                                         Human; foam cell differentiation; atherosclerosis; cerebral stroke; cardiovascular disorder; coronary artery disease; gene therapy; ds.
                                                                                                                                                                                                    Porter GJ,
                                                                                                                                                                                                    Seilhamer JJ,
                                                                                                                                                                                                     Α,
                                                                                                                                                                                                      Lawn
                                                                                                                                                                                 (INCY-) INCYTE GENOMICS INC.
                                                                                                                                             04-APR-2001; 2001WO-US11128.
                                                                                                                                                               05-APR-2000; 2000US-195106P.
                         (first entry)
                                                                                                                                                                                                    Shiffman D, Somogyi R,
                                                                                                                                                                                                                                WPI; 2002-010925/01.
                                                                                                         WO200177389-A2
                        14-FEB-2002
                                                                                         Homo sapiens.
                                                                                                                           18-OCT-2001.
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Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome polymerase chain recombinant production of (II). The configuration recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and and contraction of mutations and the produce other types of data and products dependent on DNA and and and an order the contract of the produce other types of data and products dependent on DNA and and an order the polyperide and produce other types of data and products dependent on DNA and and an order the polyperide sequences. ABS4654 represent novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    printed
from WIPO
                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not appear in the specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1539 BP; 396 A; 379 C; 347 G; 417 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 20764; 103pp; English
                                                                                                                                                                                                                                                     Tang YT;
                                                                                                                         2000US-0540217.
2000US-0649167.
                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                 WPI; 2001-639362/73.
P-PSDB; ABG20773.
                                                                                                                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                         31-MAR-2000;
                                                                                                                                                23-AUG-2000;
                          11-0CT-2001
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   Length 1539;
                             16;
                           21; Indels
 DB 23;
               Pred. No. 0;
0; Mismatches
Score 1281.4;
Pred. No. 0;
Query Match 83.4%;
Best Local Similarity 97.4%;
Matches 1410; Conservative
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286 1359 346 1299 406

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1479 226

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1239 CTGTCTTCCAAGGGAGTGAAAATCTGGGATGCCAATGGATCCCGAGACTTTTTGGACAGC 1180
                                               1059 CIGCAAAGAGIGAITIGACACCAICAAAACCAACCTGACGACAGAAGAAICAICAITIGC 1000
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New antisense oligonucleotides directed against thymidylate synthase
                                                                                                                                                                                                                                                                                       tumour cell; anticancer drug; treatment; cancer; antiproliferative; anticoestrogen; progestogen; antiandrogen, testosterone inhibitor; anti-invasion agent; growth factor inhibitor; antimetabolite; antibiotic; alkylating agent; antimitotic agent; radiotherapy;
                                                                                                                                                                                                                                                                 Ihymidylate synthase; antisense oligonucleotide; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dean NM, Koropatnick DJ, Vincent MD;
                         AAX24270 standard; DNA; 566 BP.
                                                                                                                                                                                                        Human thymidylate synthase DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                    topoisomerase inhibitor; ss.
                                                                                                                                             02-JUL-1999 (first entry)
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                                                                                                             The present invention provides a novel method of estimating the susceptibility of an individual to a developmental disorder using genetic and environmental variables. The method can be used in the diagnosis, prevention and treatment of disorders such as schizophrenia, spina bifida cystica, Tourette's syndrom, bipolar illness, autism, conduct disorders, attention deficit disorder, obsessive compulsive disorder, chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agactttcagattgaagggtacaatccgcatccaactattaaaatggaaatggctgttta 15749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 613.2; DB 22; Length 18596;
Pred. No. 2e-149;
0; Mismatches 63; Indels 6;
                                                                                                                                                                                                                                                                          attention deficit disorder, obsessive compulsive disorder, chi
multiple tic syndrome and learning disorders such as dyslexia
                                                                                                                                                                                                                                                                                                                                                                  Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;
                                                           Disclosure; Page 125-131; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 39.9%;
Best Local Similarity 90.6%;
Matches 667; Conservative (
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                                                            This invention describes novel antisense oligonucleotides targeted to sequences in the 3' end of thymidylate synthase (TS) mRNA. Such oligonucleotides are cytostatic on their own when administered to human tumour cell lines, and also enhance the toxicity of anticancer drugs such as Tomudex administered to those cells. In addition, antisense oligonucleotides targeted to 5' sequences induce TS gene transcription. The antisense oligonucleotides are used in a method for the
                                                                                                                                                                                                                                                                                                                                                                        The antisense oligonucleotides are also used in the production of a medicant for the treatment of cancer, either separately or in conjunction with a therapeutic agent such as thymidylate synthase (TS) inhibitors
                                                                                                                                                                                                                                                                                                                                treatment of cancer (or a method for providing antiproliferative effect)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agents (e.g. antioestrogens, (anti)progestogens, antiandrogens, testosterone inhibitors, anti-invasion agents, growth factor inhibitors, etc.); antiproliferative/antineoplastic agents (e.g. antimetabolites,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.6%; Score 501.2; DB 20; Length 566; 99.4%; Pred. No. 6.7e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antitumor antibiotics, alkylating agents, antimitotic agents,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                topisomerase inhibitors, etc.), or radiotherapy
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Disclosure; Fig 7; 53pp; English.
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                                                            19102 aattoatacaatgggggatgcacatatttacttgaatcatatagatgctttaaaagtgca 19161
                                                                                                                                                                                                                                                                                                                                                                                                 19162 gctagctcgatccccaaaaccttttccttgccttaaaattattcgaaatgtaacagatat 19221
                                                                                                                                                                                                                                                                                                                                                                                                                                                             18862 taaaaccaaaacccagaaagccgacgaatgattatatcgtcttggaatccaaaggatatccc 18921
                                                                                                                                                                                                                         tgatgacttcaaagctgaagactttcagattgaagggtacaatccgcatccaactattaa 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca mulatta rhadinovirus 17577; RRV; rhesus macaque rhadinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a novel rhesus macaque rhadinovirus
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                                         tetgatggegetgeeteeatgeeatgeeetetgeeagttetatgtggtgaacagtgaget
                                                                                                                      gteetgeeagetgtaccagagatcgggagacatgggcetcggtgtgcetttcaacatcge
                                                                                                                                                                                                                                                                               849 tatacacactttgggagatgcacatatttacctgaatcacatcgagccactgaaaattca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions associated with RRV infection
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                                                                                                                                                                                                                                                                                                                                                                                                                              Method for checking absence of mutation at specific positions of varicella virus genome for quality control of attenuated live varicella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18442 cggcgaacttcagtacttaaaacaagtggatgatattttaaggtatggagttcggaaacg 18501
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                                                                Oka strain; pox vaccine; vaccine; poxvirus disease; chickenpox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 125157;
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                          of the Varicella virus Oka strain.
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Pred. No. 2.1e-95;
                                                                                                                                                                                                                                                                                                                                                 Yamanishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 106-150; 158pp; Japanese.
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66.5%;
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                                                                                                                                                                                                                                                                   31-JAN-2000; 2000JP-0062734
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                             Nucleotide sequence
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                                                                                                       Zaricella virus
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Score 387.4; D
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Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2; dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis; diagnosis; treatment; HHV8; complement binding protein: vCBP; SSBP; ssDNA binding protein; transport protein; glycoprotein B; pol; vIL-6; DNA, polymerase; viral interleukin-6; BHV4-IEI I; thymidylate synthase; vMIP-II; BHV4-IEI II; vMIP-I; capsid protein I; tegument protein I; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              capsid protein I, ORF18 and ORF19 which encodes Tegument protein I. KSHV is a new human Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common form of neoplasm occurring in persons with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for K1, ORF4 which encodes the complement binding protein vocabe, ORF6 which encodes a ssDNA binding protein (SSBP), ORF7 which encodes a transport protein, ORF8 which encodes glycoprotein B, ORF9 which encodes DNA polymerase (pol), ORF10, ORF11, K2 which encodes viral interleukin c (vIL-6), ORF02 which encodes dlydrofolate reductase (DHFR), K3 which encodes WHV4-IEI I, ORF70 which encodes Thymidylate synthase, K4 which encodes WHP-II, K5 which encodes BHV4-IEI II, K6 which encodes BHV4-IEI II, K6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acquired immune deficiency syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma and for detecting expression of a DNA virus associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21023 GECGICIIGGCITIGGCCCCCGAGGIIGACCCIIGIICGAIICAGCAIGAGGIAACIGGG 20964
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.larity 63.5%; Pred. No. 2.7e-90;
Conservative 0; Mismatches 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moore PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Column 67-96; 109pp; English.
                                                                                                                                                                                                                                                                                                           Kaposi's sarcoma-associated herpesvirus.
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                                                                                                                  XSHV LUR DNA (nucleotides 1-35,100)
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nes 592;
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RESULT 10

the Kaposi's sarcoma-associated herpes virus (KSHY), KSHY is also known as human herpes virus (KSHY), KSHY is also known as human herpes virus 8 (HHV8). This sequence contains the DNAs of the invention which encode KSHY polypeptides selected from: (a) viral contains the DNAs of the invention which encode KSHY polypeptides selected from: (a) viral macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6); (c) viral IRP I; (d) complement-binding protein; glycoproteins B, M or Li, (d) capsid protein IV encoded by ORF65; and (e) immediate early protein encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by It, and antibodies (Ab) specific for the proteins are useful for detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body filuds or tissue samples. HHV8 infections can be treated with antisense or triplex forming molecules or agents that bind specifically to the protein. Ab may be used for prophylaxis or treatment of HHV8 infection, while the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHV8 may be implicated in many other lymphoproliferative diseases such as lymphomas, leukaemia, other lymphoproliferative diseases such as lymphomas, leukaemia, cother lymphoteid for drug screening. HHV8 derived peptides can be inhibited with methotrexate. These can also be used to determine can be inhibited with methotrexate These can also be used to determine the immune status of a patient infected with HIV. HHV8 derived protein certification frammatoid arthritis. This sequence is stated as containing for the c sequence represents the long unique region and terminal repeat of open reading frames

Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;

ó GCGGCGTACGTGGACGCGGGATGCTGACTATACAGGCCAGGGGTTTGACCAATTGTCGTAC 20544 20543 ATTGTGGATTTAATAAAAAATAATCGCACGATAGAAGAATCATTATGTGTGCGTGGAAC 20484 20483 CCGCCGGACTTGTCGTTGATGCCGCTTCCGCCCTGTCACTTGTTATGTCAATTTTATGTA 20424 21023 GOCGICTIGGCTTIGGCCCCCGAGGTIGACCCTIGTICGATICAGCATGAGGTAACTGGG 20964 20663 GCGCACAGAAGGGAGGGGGATTTGGGACTGTTTACGGTTTCCAGTGGAGGCACTTTGGG 20604 115 geoggetoggagetgeogegeoegtegeeettgeeecoggegeacaggaggaeggeegag 174 175 ccgcgtccgccgcacggggagctgcagtacctgggggcagatccaacatcctccgctgc 234 295 cgctacagcctgagagatgaattccctctgctgacaaccaaacgtgtgttctggaagggt 354 355 gtttttggaggagttgctgtggtttatcaagggatccacaaatgctaaagggctgtcttcc 414 aagggagtgaaaaatctgggatgccaatggatcccgagactttttggacagcctgggattc 474 0; Gaps 20963 GCTGAGACGCCCCACGAGGAACTICAGTATCTCAGGCAGTTGAGGGAAATTTTGTGCCGT ggogtcaggaaggacggcacgggcaccggcaccggcaccctgtcggtattcggcatgcaggcg 20843 AGGIAIAGICIGGGGACCACITICCCITACIAACCACAAAGCGGGIGTITIGGCGAGGC tecaccagagagagagagtttggggcccagtttatggcttccagtggaggcattttggg gcagaatacagagatatggaatcagattattcaggacagggagttgaccaactgcaaaga gtgattgacaccatcaaaaccaaccctgacgacagaagaatcatcatgtgcgcttggaat Score 387.4; DB 19; Length 137507; Pred. No. 5.2e-90; Indels 0; Mismatches 341; Query Match 25.2%; Best Local Similarity 63.5%; Matches 592; Conservative (415 475 655 535 20603 235 g g g g g δŏ g QΣ g δŽ g δŽ δŏ g δ δ δ δŽ

715 gtgaacagtgagctgtcctgccagctgtaccagagtcgggagacatgggcctcggtgtg 774

δŽ

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO ed nucleic acid detection reagent for detecting 1000 or more Drosophila and for elucidating cell signalling and cell-cell 20423 GCTGACGGTGAGCTTTCCTGTCAGCTGTATCAGAGGTCGGGAGACATGGGTTTGGGAGTT 20364 20183 TCTGTTTCTTCCATGGAAGAGTTTACACCTGATGATTTTAGACTGGTGGACTACTGCCCG 20124 capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of 20303 AGACCCGGGGGGTTTATTCACACGTTGGGAGATGCCCACATCTACAAAACGCATATAGAG 20244 The invention relates to an isolated nucleic acid detection reagent insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA 20243 CCACTACGGCTGCAGCTGACGCGCACTCCACGTCCCTTTCCGCGCCTGGAGATACTCCGG 955 aaagttgagaaaattgatgacttcaaagctgaagacttcagattgaagggtacaatccg cettteaacategecagetacgecetgeteacgtacatgattgegeacateacgggeetg 835 aagccaggtgactttatacacactttgggagatgcacatatttacctgaatcacatcgag 895 ccactgaaaattcagcttcagcgagaacccagacctttcccaaagctcaggattcttcga Drosophila melanogaster expressed polynucleotide SEQ ID NO 11762. developmental biology; cell signalling; insecticide; Claim 1; SEQ ID NO 11762; 21pp + Sequence Listing; English. (ABL01840-ABL16175) and the encoded proteins at ftp.wipo.int/pub/published_pct_sequences. 20123 CATCCTACCATTCGTATGGAAATGGCAGTATAG 20091 1015 catccaactattaaaatggaaatggctgtttag 1047 EW; Myers discloses genomic DNA seguences PWD, ABL05760 standard; cDNA; 2966 23-MAR-2001; 2001WO-US09231. 2000US-191637P. 2000US-0614150. (first entry) Ë pharmaceutical; gene; ss. Drosophila melanogaster. Venter JC, Adams M, ABB57737-ABB72072). WPI; 2001-656860/75. (PEKE) PE CORP NY. P-PSDB; ABB61657 WO200171042-A2. 23-MAR-2000; 11-JUL-2000; New isolated interactions 27-SEP-2001. 26-MAR-2002 Drosophila; qenes from ABL05760; 12 775 ABL05760 g ద g qq δŽ δy g 임 δŏ QY QΫ́

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Human; immunotherapy; diagnosis; colon cancer; colon tumour;
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406 gatctggggccggtgtacggcttccaatggaggcatttcgggggcgcagtacggcactgc 465
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                  gocagotacgccctgctcacgtacatgattgcgcacatcacgggcctgaagccaggtgac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon tumour polypeptide; tumour antigen; cancer; vaccine; otherapy; diagnosis; progression; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA encoding human colon tumour polypeptide, SEQ ID NO:443.
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                                                                                        673 atggcgctgcctccatgccatgccctctgccagttctatgt---
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99US-0347496.
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, Yuqiu J;
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02-JUL-1999;
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Sequences AAAI/12-AV319 represent 470 chars encounty process. Sequences AAAI/12-AV319 represent 470 chars encount process. The invention also specifically discloses 8 human colon tumour proteins antigen presenting cells (APCs, preferably dendritic cells) expressing cantigen presenting cells (APCs, preferably dendritic cells) expressing such polypeptides may be used in vaccines that target tumour cells, cancer 1-cells specific for the polypeptide expressed by the APC are used to remove tumour cells, thereby inhibiting the development of fractions thereof. The sample or the isolated T-cells specific for the polypeptide cancer development. Code and/or CPS polypeptide can then be used to inhibit cancer development. Code and/or codes the proliferation of specific T-cells from be polypeptides or nucleic acid of the invention, or an APC expressing such a polypeptide or nucleic acid encoding the polypeptides and antibodies and then administrated back to the patient to inhibit cancer cancer cells are present. Such diagnostic methods may also be used to attend mour protein of the invention, and therefore to determine whether cancer cells are present. Such diagnostic methods may also be used to monitor the progression of a cancer by repeating the processes at time intervals, and comparing the current result to preventious results. The intervals.
New colon tumor polypeptides used to inhibit the development of cancer, especially colon cancer, and for diagnosing and monitoring the progression of the cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1187 aggatgttgccactggcaaatgtaactgtgccagttctttccataataaaaggctttgag 1246
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                                                                                                                                                                              AAA77722-A78199 represent 478 cDNAs encoding proteins
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Pred. No. 8.8e-79;
0; Mismatches 4; Indels 0;
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                                                                                                                         Claim 1; Page 218; 229pp; English.
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Series: IRAL Plate: 4 Row: h Column: 10
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BIR71083 603394256
BM457044 AGENCOURT
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BM413631 AGENCOURT
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AKO11435 Mus muscu
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BF690478 602186947
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Contact: nisc_mgcBnhgi.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspl,R.,
Lim,M., Maduro,Q.L., Mastelallo,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                 BG575942 602598373
                                              BM467591 AGENCOURT
                                      BI859272 603385476
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                             BM472540 AGENCOURT
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Mammaila; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1533)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                             linear
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Homo sapiens, clone IMAGE:3141419, mRNA.
BC018858
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BI871083
BM457044
AL548721
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BI85272
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                             Strausberg, R.
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Copyright (c) 1993 - 2000 Compugen Ltd
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 /clone_lib="LTI_NFL006_PL2"
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//note="Vector: pCNVSpORT 6; Site_l: Not!; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCNVSpORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 8900 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371.
Email: fliang@lifetech.com URL
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253 c 217 g 318 t
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Pred. No. 2.1e-225;
2; Mismatches 7;
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cloned into the Not I and Eco RV sites of the pCMNSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fullength.invitrogen.com; 9 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="placenta" //tissue_type="placenta" //note="Yector: pCHNYSPORT 6; Site_1: NotI; 1st strand cDNA was primed ** Five prime end was primed ** Five prime end enriched, double-stranded cDNA was digested with Not I and enriched, double-stranded cDNA was digested with Not I and
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
CTGTGCCAGTTCTTTCCATAAAAGGCTTTGAGTTAACTCACTGAGGGTATCTGACAA
                                                DB 9; Length 1077;
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/clone="cs0b1008YH21"
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                              seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                           coctotgccagttctatgtggtgaacagtgagctgtcctgccagctgtaccagagtcgg
 tccagtggaggcattttgggggcagaatacagagatatggaatcagattattcaggacagg
                                                      tttacctgaatcacatcgagccactgaaaattcagcttcagcgagaacccagacctttcc
                         481 TCCAGTGGAGGCATTTTGGGGCAGAATACAGAGATATGGAATCAGGATTATTCAGGACAGG
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Mammalia, Eutheria, Primates, Catarrhini, Hon
1 (bases I to 1021)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/lab_host="DH10B"
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BP 191 91006 EVRY cedex - France
Email: seqref@qenoscope.cns.fr, Web : www.
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/db_xref="taxon:9606"
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AL562750
AL562750.1 GI:12911478
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AUTHORS
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                                                                                               Length 1021;
                                            others
  Fax
                                                                                                                              Indels
 Drive Rockville, Maryland 20850, USA 8371 Email : fliang@lifetech.com URL
                              http://fulllength.invitrogen.com"
230 c 203 g 307 t
                                                                                               Score 945.2; DB 9;
Pred. No. 2.9e-202;
3; Mismatches 16;
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nilarity 98.0%;
Conservative 3
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AL551990.1 GI:12890459
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Pred. No. 1.5e-199;
4; Mismatches 0; Indels
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99.6%;
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was primed with a Notrolly (dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Context: Feng Liang Life Technologies. Context: Feng Liang Life Technologies. Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fullength.invitrogen.com "I others" of 259 g. 188 t. 1 others
                                                                                                                                                                                                                                                                                                 AL551990 ALT. NFL006_PL2 Homo sapiens cDNA clone CSODIO60YE04 5 prime, mRNA sequence.
AL551990
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/clone_its="LTI_NFLOOG_FL2"
/tissue_type='placenta"
/note="Vector: pCWVSPORT 6; Site_1: Not!; 1st strand cDNA
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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Pred. No. 3.2e-199;
                                                                                                                                                 1; Mismatches
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Mammalia; Eutheria; Primates;
1 (bases 1 to 938)
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180 282 240 342 360 462 522 480 582 540 642 900 702

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932 bp mRNA linear BST 13-FEB-2001
Homo sapiens cDNA clone CSODC018YA14 5
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Catarrhini; Hominidae; Homo.
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                      CGGGACGCCGAGCCGCCCCCCCCCCCCGGGGAGCTGCAGTACCTGGGGCAGATCCAACAC
                                                                                                                                                                                                gagotgtcttccaagggagtgaaaatctgggatgccaatggatcccgagactttttggac
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Mammalia; Eutheria; Primates;
1 (bases 1 to 932)
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AL526821 LTI_NFL003_NBC3
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AL526821
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/tissue_lype="placenta"
/tissue_lype="placenta"
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/tissue_type="placenta"
/tissue_type="placenta"
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Email: filliang@lifetech.com URL :
http://fullength.lnvitrogen.com"

20 a 274 c 261 g 189 t 6 others
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Homo sapiens CDNA clone CSODI056YE24 5
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1. (bases 1 to 950)

Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

Full-length, CDNA libraries and normalization
                                                                                                                                        963 gaaaattgatgacttcaaaggctgaagactttcagattgaagggtacaatccgcatccaac 1022
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                                                                                        903 aattcagottcagogagaacccagacctttcccaaagctcaggattcttcgaaaagttga 962
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/db_xref="taxon:9606"
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AUTHORS NIH-MGC http://mgc.nci.nih.gov/. IIILE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Extrasberg, Ph.D. Email: cgapbs-rémail.nih.gov Tissue Procurement: Lou Staudt CDNA Library Preparation: Life Technologies, Inc. CDNA Library Prayed by: The I.M.A.G.E. Consortium (LINL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.gov Plate: LLAM12268 row: g column: 17 High quality sequence stop: 687. High quality sequence stop: 687.		Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library." BASE COUNT 242 a 297 c 286 g 220 t		Qy 33 ccogcogogcacttggcctgccgtccggcgcgcgccacttcgcctccgtcccc 92	Qy 93 egocogocoatgootgtggcoggotocgaqocogocococococococococococococococococo	Oy 153 ogcacaggagogogacgcogagocgcoccacaggagagcactggggca 212	Oy 213 gatecaacatectecgetgeggegteaggaaggaegaeegggeaeegt 272 	Oy 273 gtcggtattcggcatgcaggcggctacagctgagagatgaattccctctgctgacaac 332	Qy 333 caaacgtgttctggaaggtgttttggaggagttgctgtggttatcaagggatccac 392 	393		Oy 513 cttccagtggaggcattttggggcagaatacagagatatggaatcagattattcaggaca 572 	Qy 573 gggagttgaccaactgcaaagagtgattgacaccatcaaaaccaacc
	366 301 426 361	OY 48b agaaggagaactaggaccagtraagggatrocagraggagaar. 421 AGAAGAGGACTTGGGCCAGTTTATGGCTTCCAGTGGAGGCAATACAG 480 Db 421 AGAAGAGGACTTGGGCCCAGTTTATGGCTTCCAGTGGAGGCATTTGGGGCAGAATACAG 480 Oy 546 agatatggaatcagattattcaggacagggagttgaccaactgcaaagagtgattgacac 605 Oy 648 agatatggaatcagattattcAGGACAGGGGATTTGTTGAGAACTGCAAAGAGTGATTGACAC 540	Oy 606 catcaaaaccaaccctgacgacagaagaatcatcatgtgcgcttggaatccaagagatct 665	Oy 666 teetetgatggegetgeeteeatgeeatgeeetetgeeagtetatgtggtgaacagtga 725 	Qy 726 gotgtoctgccagotgtaccagagatcgggagacatgggcctcggtgtgcctttcaacat 785	Oy 786 ogccagotacgccctgctcacgtacatgattgcgcacatcacgggcctgaagccaggtga 845 	Oy 846 cittatacacactttggggagatgcacatatttacctgaatcacatcgagccactgaaaat 905 	Oy 906 toagottcagogagaacocagacotttoccaaagotcaggattottcgaaaagttgagaa 965 	Oy 966 aat 968 	1045 bp	on AcenCOUKT_0486220 NIH_MGC_65 Homo sapiens cuna 5', mRNA sequence. The MA478045.1 GI:18527087	5	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1045)

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Search completed: July 26, 2002, 15:13:16
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http://fullleagh.invitrogen.com "3 others
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                             AL578646 AL7_NFLO06_PL2 Homo sapiens CDNA clone CSODK004YL08 3
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1 (bases 1 to 906)

11,Was. Gruber,C., Jessee,J. and Polayes,D.

Full-length CDNA libraries and normalization
Unpublished (2001)

Contact: Genoscope
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BP 191 91006 EVRI cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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BC020139 Mus muscu
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M30774 Mouse thymi
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M86409 Herpesvirus
X64346 Herpesvirus
M14080 Herpesvirus
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AX330682 Sequence
AX330906 Sequence
AX33755 Sequence
D00596 Homo sapien
AF305057 Homo sapien
AC021474 Homo sapi
AC020697 Homo sapi
AX341901 Sequence
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                                                                  July 26, 2002, 09:55:26; Search time 5000.16 Seconds
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           GenCore version 4,5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                         1797656 segs, 10463268293 residues
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Listing first 45 summaries
                                                 OM nucleic - nucleic search, using sw model
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Homo sapiens, thymidylate synthetase, clone MGC:1590 INACE:3138877, mRNA, complete cds. BC002567 BC002567.1 GI:12803482 MGC.
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MGLGYPFNIASYSALLTYMTAHITGLRRGDFIHTGDAHTILNHIEPLKIQLQREPFP
PKLRILRKVEKIDDFKAEDFQIEGYNPHPTIKMEMAV"
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1519. .1524
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369 c 399 g 378 t
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Matches 1533; Conservative
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Dp		δλ	382 aagggatccacaaatgctaaagagctgtcttccaagg
QY	1356 tataaagaaggttggtgaatttcacaagctatttttggaatatttttagaatattttaag 1415 	Db Qy	361 AAGGGTCCACAAATGCTAAAGAGCTGTCTTCCAAGG 442 ggatcccgagactttttggacagoctgggattctcoa
δŽ	aatttcacaagctattccctcaaatctgaggagctgagtaacaccatcgatcatgatgt	qq	
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RESULT AX281791 LOCUS DEFINITIC	4 X	oy oy	601 GACGACAGAAGAATCATCATGTGCGCTTGGAATCCAA 682 cctccatgccatgccagttctatgtggtga
ACCESSION VERSION KEYWORDS SOURCE	AX281791 AX281791.1 GI:16609042 human.	QY	742 taccagagatoggagacatgggoctoggtgtgcctt
OR		oy 4	
REFERENCE AUTHORS TITLE JOURNAL		g ZZ	/81 CTCACGTACATGCCCACATCACCGCCCTGAACC 862 ggagatgcacatatttacctgaatcacatcgagccac 841 [
FEATURES SOU	Incyte Genomics, Inc. (US) Location/Qualifiers I3298 Arranism-Homo sanians'	00 بر دار	
BASE C ORIGIN	/db_xref="feacon:9606" /note="Incyte ID No: 247220.15" COUNT 898 a 709 c 744 g 919 t 28 others	QY	
Que Bes Mat	Query Match 97.3%; Score 1494.8; DB 6; Length 3298; Best Local Similarity 99.4%; Pred. No. 1.66-299; Matches 1512: Conservative O. Misematches 3. Tridels 6. Gans 1.	Qy	1042 gtttagggtgctttcaaaggagctCgaàggatattgt
λο ₄ ο	Gacageacacttagectgcctccqccacacacttcgcctg 81	QY	1102 tgccgaggtaaaagttctttttgctctaaaagaaGaa
S & dd	Control Cont	QY	1162 gtgacctatcagttattaatttttaaggatgttgcca
Oy Oy		QY	1222 totttocataataaaagotttgagttaactoactga
QY Dp	tacctggggcagatccaacacatcctcggctgcggcgtcaggaagga	QY Db	1282 atgaacaaagtgaggagaatgaaatgtatgtgctctt
QY	accggcaccctgtcggtattcggcatgcaggcgcctacagcctgagagatgaattccct	Oy Dp	1342 caatcccacgtacttataaagaaggttggtgaatttc
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	RESULT 6 AX069365 LOCUS DEFINITION Sequence 29 from Patent W00102600. DEFINITION SAUGES 5. AX069365.1 GI:12579227 VERSTON AX069365.1 GI:12579227 NAMMAN. NAMMAN. ORGANISM Homo sapiens ENERTYCKE, Westsoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. ORGANISM Homo sapiens ORGANISM Homo sapiens ENERTYCKE, Words 1 to 942 AUTHORS TITLE AUTHORS TITLE AUTHORS Location of analytes using attenuated enzymes JOURNAL ATOMICS (US) FRATURES LOCATION (Walifiers LOCATION (Walifiers LOCATION (Walifiers 1. 0442 AUTHORS HOMO sapiens" ADAMORNAL AUTHORS HOMO sapiens" ADAMORNAL AUTHORS HOMO sapiens" AUTHORS HOMO Sapiens HOMO Sapien

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Mouse, cDNA to mRNA, clone pMTS-3.
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38. .961</pre>
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FNIASYALLYMTAHITGLQPGPFVHTLGDAHIYLNHIEPLKIOLQREPRPFPKLKIL
RKVETIDDFKVEDPGTXVPHPTIKNEMAV"
1 226 c 253 g 237 t
                                                                                                                                                                                                                              TGTGTLSVFCMQARYSLRDEFPLLTTRRVFWRCVLEELLWFIKGSTNAKELSSKGVRI
WDANGSRDFLDSLGFSARQEGDLGPVYGFQWRHFGAEYKDMDSDYSGQGVDQLQKVID
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                                                                                                                                                                                                                 /translation="MLVVGSELQSDAQQLSAEAPQHGELQYLRQVEHILRCGFKKEDR
/db_xref="taxon:10090"
/clone="MGC:28246 IMAGE:3994204"
/tissue_type="Mammary tumor metastatized to lung. Tumor arose spontaneously from a senescent normal mammary (clonal) outgrowth infected with the virus MMTV."
/lab_bost="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 gagagatgaattccctctgctgacaaccaaacgtgtgttctggaagggtgttttggagga 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             546 agatatggaatcagattattcaggacagggagttgaccaactgcaaagagtgattgacac 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               catcaaaaccaaccetgacgacagaagaatcatcatgtgcgcttggaatccaagagatct 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   352 AATCTGGGATGCCAATGGATCCCGAGATTTTCTGGACAGCTTGGGATTTTCTGCCCGACA 411
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGAGATGAATTTCCTCTCTCTCACAACCAAACGAGTGTTCTGGAAGGGTGTTTTGGAGGA
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                                                                                                                                                                                                                                                                                                                                                                          46.3%; Score 711.4; DB 10; Length 986; 85.8%; Pred. No. 3.5e-137;
                                                                                                                                                               /product="Unknown (protein for MGC:28246)"
/protein_id="AAH20139.1"
/db_xref="GI:18044897"
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 131;
                                                                                                               /note="Vector: pCMV-SPORT6"
50. .973
                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                           790; Conservative
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/processionid=124AA40439.1"
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/translation="MLVVGSELQSDAQQLSAEAPRHGELQYLRQVEHILRCGFKKEDR
/translation="MLVVGSELQSDAQQLSAEAPRHGELQYLRQVEHILRCGFKKEDR
TGTGTLSVFGMQARYSLRDEFPLLFTKRVFWKGVLEELLWFIKGSTNAKELSSKGVRI
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TIKTNRPDRRIINGANNFKDLPHAALPPCHALCQFVYVNGELSCQLYQRSGDMGLGVP
FULASYALLTYMIAHITGLQPGDFVHTLGDAHIYLNHIEPLKIQLQREBPFFFFKIKIL Draft entry and printed copy of the sequence [1] kindly provided by L.F.Johnson, 29-AUG-1986. ROD 27-APR-1993 Perryman, S.M., ROSSana, C., Deng, T., Vanin, E.F. and Johnson, L.F. Sequence of a CDNA for mouse thymidylate synthase reveals striking similarity with the prokaryotic enzyme Mol. Biol. Evol. 3, 313-321 (1986) Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 961) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; aattgatgacttcaaagctgaagactttcagattgaagggtacaatccgcatccaactat 1025 getgeegeeggeeettgeeeeegeegeaaggaagggaegeegageegegteegee 185 100 gcargeagaacrecagracergagecaggregageacaerrrrecgergeggerreagaa 159 905 965 771 831 891 951 40 ecreerectrecarecrecarecrearecreacreacreacececeaagececare 99 gcacggggagctgcagtacctggggcagatccaacacatcctccgctgcggcgtcaggaa tcagcttcagcgagaacccagacctttcccaaagctcaggattcttcgaaaagttgagaa 0; Length 961; /note="thymidylate synthase (EC 2.1.1.45)" Mouse thymidylate synthase mRNA, complete cds. M13019 M15191 GI:202029 thymidylat. Indels .6; DB 10; 3.4e-136; RKVETIDDFKVEDFQIEGYNPHPTIKMEMAV"

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524 CGACAGGAAGGGGACCTGGGCCCCAGTTTATGGTTTCCAATGGAGGCATTTTGGAGCAGAG 583
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Sequence 11 from patent US
AR144965
AR144965.1 GI:15106832
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MOUSE thymidylate synthase pseudogene mRNA, complete cds.
M30774
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                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammala, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I. (bases 1 to 1349).
Li,D. and Johnson,L.F.
                                                                                                                  gagaaaattgatgacttcaaagctgaagactttcagattgaagggtacaatccgcatcca 1020
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                                                                                                                                          838 GAGACAATCGATGATTTCAAAGTTGAAGACTTTCAGATTGAAGGGTATAATCCACATCCA 897
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                464 Greagarcressarscraaragarcccsasacrrresacaccressarrrrcrecc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="pseudo-thymidylate synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.3%; Score 634.2; DB 10
84.6%; Pred. No. 3.5e-121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             349
                                                                                                                                                                                                                                                                                                  pseudogene; thymidylate synthase.
Mouse LU3-7 and 3T6 cell line DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 a 320 c 335 g upstream of HindIII site.
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1. .1349
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1 (bases 1 to 18596)
Johnson, W.G. and Stenroos, E. Scott.
Methods for diagnosing, preventing, and treating developmental
disorders due to a combination of genetic and environmental factors
Patent: US 6210950-A 11 03-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 08-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 15510 GAACTTTGTTGATCACATCCTGTGTACTTTCACGGACATGAGGAGCAATTACAACAG 15569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           947 ttettegaaaagttgagaaattgatgaetteaaagetgaagaettteagattgaagggt 1006
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                                                                                                                                                          tacagagatatggaatcagattattcaggacagggagttgaccaactgcaaagagtgatt
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BASE COUNT

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Young.P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
                                                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15510 GAACTITGITGATCACATCCTGIGIACIIGITTCACGGACAIGAGGAGCAATTACAACAG 15569
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                                                                                                                                                             Patent: WO 0194629-A 1415 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
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                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
3991 c 4479 g 560
                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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              Patent: WO 0194629-A 1191 13-DEC-2001;
Avalon Pharmaceuticals (US)
Location/Qualifiers
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                                                             1. .18596
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 1176;
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Sequence 1, Appli
Sequence 42, Appl
Sequence 59, Appl
Sequence 5, Appli
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Sequence 3, Appli
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Sequence 7, P
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
                                                                                              July 26, 2002, 17:46:36 ; Search time (without 3753.437
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US-08-481-485-5

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US-09-347-114A-71

US-08-347-114A-71

US-08-116-001-6

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US-09-154-602-6

US-09-154-602-6

US-09-154-602-6

US-09-157-681-45

US-09-157-681-45

US-09-268-992-7

US-09-480-784-20

US-08-480-784-20

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US-08-646-301A-1
US-08-481-968A-4
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Listing first 45 summaries
                                                                   - nucleic search, using sw model
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GenCore
Copyright (c) 1993
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US-08-154-712B-4
US-09-813-817-3
US-08-781-891-79
US-08-969-125-8
US-08-848-252-1
PCT-US93-06251-80
PCT-US93-06251-80
US-08-09-33-33-3
US-08-09-11-1
US-08-09-11-1
US-09-033-333-2
US-08-257-963B-11
US-09-033-333-2
US-08-257-963B-11
US-09-033-331-2
US-08-257-963B-11
US-09-033-331-2
US-08-257-963B-11
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US-09-033-331-2
US-08-257-963B-11
US-09-033-331-2
US-08-257-963B-11
US-08-257-963B-11
US-08-257-963B-11
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APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PR.
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
CURRENT APPLICATION UNDER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
                                                                                                                                                                                  US-08-434-998-8
                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                           02-09-318-448-11
Sequence 11, Application US/09318448
Patent No. 6210950
; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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182
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16.2%; Score 191.8; DB 4; Length 15977; 77.1%; Pred. No. 1.8e-25;
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                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/608,285A CURRENT FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: 09/583,231
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PRIOR APPLICATION NUMBER: 09/557,800

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

PRIOR PELING DATE: 2000-01-11

PRIOR FILING DATE: 1099-08-09/81,238

PRIOR PILING DATE: 1999-07-16

PRIOR APPLICATION NUMBER: 09/370,265

PRIOR APPLICATION NUMBER: 09/370,265

PRIOR APPLICATION NUMBER: 09/350,836

PRIOR FILING DATE: 1999-07-19

PRIOR PILING DATE: 1999-07-09

PRIOR APPLICATION NUMBER: 09/273,447

PRIOR FILING DATE: 1999-02-04

PRIOR FILING DATE: 1999-07-24

PRIOR APPLICATION NUMBER: 09/118,205

PRIOR FILING DATE: 1998-07-24

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LOCATION: (14871)
OTHER INFORMATION: n = a or c or g or t
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            ENERAL INFURENCE....
APPLICANT: Ford, John
APPLICANT: Mulero, Julio
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            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: n = adenosine or guanine or cytosine or thymidine US-09-608-285A-42
                                              TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE TITLE OF INVENTION: POLYPEPTIDES FILE REFERENCE: 28110/36570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 10288 egegeetggeecetattecactettetaagagaaaateetaca 10332
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PRIOR APPLICATION NUMBER: 09/481,238

PRIOR FILING DATE: 2000-04-25

PRIOR PILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: 09/370,265

PRIOR FILING DATE: 1999-08-09

PRIOR FILING DATE: 1999-07-16

PRIOR FILING DATE: 1999-07-16

PRIOR PILING DATE: 1999-07-16

PRIOR PILING DATE: 1999-07-16

PRIOR PILING DATE: 1999-07-19

PRIOR PILING DATE: 1999-07-19

PRIOR PILING DATE: 1999-07-04

PRIOR PILING DATE: 1999-07-04

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PRIOR PILING DATE: 1998-07-04
                                                                                                                      CURRENT APPLICATION NUMBER: US/09/608,285A CURRENT FILING DATE: 2000-06-30
                                                                                                                                                                    PRIOR APPLICATION NUMBER: 09/583,231
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 09/557,800
PRIOR FILING DATE: 2000-04-25
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; Patent No. 6335013
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Matches 266; Conservative
APPLICANT: Mulero, Julio APPLICANT: Yeung, George
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LENGTH: 14747
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO CD39-LIKE ITTLE OF INVENTION: POLYPEPTIDES FILE REFERENCE: 28110/36570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: KOHN & ASSOCIATES STREET: 30500 No. 6025183thwestern Highway, Suite 410
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Soreq, Hermona
APPLICANT: Zakut, Haim
APPLICANT: Zakut, Haim
APPLICANT: Shani, Moshe
IITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
TITLE OF INVENTION: AMI'-CHOLINESTERASE SUBSTNACES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 4089..22464
OTHER INFORMATION: /function= "ACHE Promotor"
OTHER INFORMATION: /standard_name= "ACHE Promotor"
                                                                                                                                                                          1007 catgoccagoctacoctttactactaatcaaagaaataa 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/814,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promotor, ACHE gene and ARS gene"
                                                                                                                                  391 cgcgtccagcgccctggcggtttttaatcaagtagaaa 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /function= "non-translated"
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cosmid including ACHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 2391.00066 TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Cosmid inc
                                                                                                                                                                                                                                                                                Sequence 7, Application US/08814095
Patent No. 6025183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (248) 539-5050
TELERAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35060 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POSITION IN GENOME: CHROMOSOME/SEGMENT: 7q22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Farmington Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
LOCATION: 22465..22537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                            US-08-814-095-7
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APPLICANT: Kent D. Taylor (Inventor)
APPLICANT: Maren T Scheuner (Inventor)
APPLICANT: Jerome I. Rotter (Inventor)
APPLICANT: Hillying Yang (Inventor)
TITLE OF INVENTION: Genetic Test to Determine
TITLE OF INVENTION: Genetic Test to Determine
FILE REFERENCE: POY 41878
CURRENT APPLICATION NUMBER: US/09/347,114A
                                                                                                                                           105 ggcggtctttttttttttttttttttttttttgggacagtcttgctcgccag 164
                                                                                                                                                                                                                                                          121 ttetectgeeteageeteegagtagetgagattataggeacetaceaceaegeeegget 180
                                                                                                                                                                                                                                                                                                                                                                                                   266 aattttgtanttttagtagagacgggggtttcaccatgttgtccaggctggtctngaac 325
                                                                                                                                                                                                                                                                                                                                                                                                                          ttottotgectcagectcccaagtag-------ccaccacgcccagct 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 gctggagtacaatggtcggatcttggctcactgcaacctctgcctcccaggttcaagcaa 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 agtacaatggtcggatcttggctcactgcaacctctgcctcccaggttcaagcaattctt 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230 ctgcctcagcctcccaagtag-----------ccaccacgccagctaattt 270
                                                                                                     42; Indels 20; Gaps
                                                                                                                                                                      110 tcttttttttttttttttttttttttgggacagtcttgctctgtgcccaggctgg 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              828 ctgtetcagceteccgagtagetggggetgcaggtgcecaccaccatgceagctaattt 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                271 ttgtanttttagtagagacggggtttcaccatgttgtccaggctggtctngaactcctg 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.9%; Score 189; DB 4; Length 3867; 77.3%; Pred. No. 5.1e-25; tive 0; Mismatches 57; Indels 20
                                                       15.9%; Score 189; DB 4; Length 631; 80.3%; Pred. No. 4.6e-25; tive 0; Mismatches 42; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 81, Application US/09347114A; Patent No. 6297014
                                                                                                   Matches 253; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 262; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 gccaccgcgtccagc 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 gecacegtgectgge 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
US-09-385-982-354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-347-114A-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OKGANISM: DOM
US-09-347-114A-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3867
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                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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1238 TITIAGIAGAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCA 1179
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                                                       ---gccaccacgcccagctaa--tttttgtan 276
                                                                                                                                                                                 277 ttttagtagaagggggtttcaccatgttgtccaggctggtctngaactcctgacctca 336
                                                                                                                                                                                                                                                                                                              337 ggtgatccacccgcctcggcccccaaagtactaggattacaggcgtgagccaccgcgtc 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 ggtoggatettggeteaetgeaacetetgeeteceaggtteaageaattettetgeetea 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.9%; Score 188.8; DB 4; Length 2713;
81.9%; Pred. No. 5.4e-25;
Live 0; Mismatches 34; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 tttttttttttttttttttttgggacagtcttgctgtcgcccaggctggagtacaat 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/154,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAB PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/916,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09154602 Patent No. 6300472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hillman, Jennifer L. APPLICANT: Lal, Preeti APPLICANT: Corley, Neil C. APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J. REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Porter Dr. CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2713 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: SCORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                238 gcctcccaagta--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-09-154-602-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  397 cagc 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-154-602-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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8622 TTTTTAGTAGAGACAGGTTTGCCATGTTGGCCAGGCTGGTCTTGAACTCCTAACCTC 8681
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             -----gccaccacgcccagctaa-tttttgta 275
                                                                                                                                276 nttttagtagaggggggtttcaccatgttgtccaggctggtctngaactcctgacctc 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: DOS
FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0367 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,901
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: RAB PROFEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08916901; Patent No. 5892012
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TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
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IBM Compatible
236 cagcctcccaagta-----
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Billings, Lucy J
REGISTRATION NUMBER: 3
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Best Local Similarity
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US-08-916-901-6/c
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EARLIER APPLICATION NUMBER: 60/078,044
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                                                                                                                                              ) NAME/KEY: modified_base
) LOCATION: all n positions
) OTHER INFORMATION: n=a, c, g, or t
US-09-268-992-7
                                                                                                                                                                                                                                                    15.8%;
73.1%;
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LOCATION: (4361)...(4507)
NAME/KEY: CDS
LOCATION: (4612)...(4737)
NAME/KEY: CDS
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Best Local Similarity 73.1:
Matches 275; Conservative
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                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                   LENGIH: 72604
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LENGTH: 8447
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                                                                                                                                       FEATURE:
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APPLICANT: Chen, H.
APPLICANT: Freimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18p RELATED DISORDERS
FILE REFERENCE: 7853-138
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.8%; Score 187.6; DB 1; Length 17327; Best Local Similarity 78.9%; Pred. No. 9.7e-25; Matches 243; Conservative 0; Mismatches 46; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
EARLIER PILING DATE: 1999-01-22
EARLIER FILING DATE: 1999-01-22
EARLIER APPLICATION NUMBER: 60/106,056
EARLIER APPLICATION NUMBER: 60/106,056
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER PILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09268992
Patent No. 6342351
TELEPAX: (202)833-8716
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                 17327 base pairs
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16397..17327
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9745..16396
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754..9596
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621..753
                                                                 NUCLEIC ACID
                                                                                STRANDEDNESS: bot
TOPOLOGY: linear
MOLECULE TYPE: DNA
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LOCATION:
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LOCATION:
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LOCATION:
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US-07-906-871-15
                                                   LENGTH:
TYPE: NU
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US-09-268-992-7
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APPLICANT: Weinshilboum, M.D., Richard M.

APPLICANT: Weinshilboum, M.D., Richard M.

APPLICANT: Wood, Thomas C.

APPLICANT: Otterness, Diane M.

TITLE OF INVENTION: SULFOTRANSPRASE SEQUENCE VARIANTS;
FILE REFERENCE: 07039/118001

CURRENT APPLICATION NUMBER: US/09/167,681A

CURRENT FILING DATE: 1998-10-07

NUMBER OF SEQ ID MOST: 52

SOFTWARE: FRASEE for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                         Score 187.2; DB 4;
Pred. No. 1.2e-24;
0; Mismatches 80;
EARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FRASEEQ for Windows Version 3.0
SEQ ID NO 7
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Search completed: \mathrm{July}\ 26, 2002, 17:48:22 Job time: 12551 sec
FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                   110 tettittittittittittittittittittigggacagiettgetetgicgeccaggetgg 169
                                                                                                                                                                                                                     52; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                         --gecaccacgcccagctaattt
                                                                                                                                                                                    Score 186; DB 4; Length 8453;
Pred. No. 1.8e-24;
0; Mismatches 52; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer TITLE OF INVENTION: Succeptibility Gene UNUMBER OF SECURACES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Venable, Baetjer, Howard & Civiletti, LLP 1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skolnick, Mark H.
Goldgar, David E.
Miki, Yoshio
Swenson, Jeff
Kamb, Alexander
Harshman, Keith D.
Shattuck Eldens, Donna M.
Tavtigian, Sean V.
Wiseman, Roger W.
Futreal, P. Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1989 cacgctcagcctctttcttgttctatat 2016
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                                                                                                                                                                                     Query Match 15.7%;
Best Local Similarity 78.0%;
Matches 256; Conservative
                                                                                                                                                                                                                                                                                                                                                                             230 ctgcctcagcctcccaagta-
                                              CDS
(6543)...(6638)
CDS
(7137)...(7316)
                                                                                                                    ; LOCATION: (7439)...(7553)
US-09-167-681-45
                    CDS ...(6447)
    (4827)...(4925)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
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                                                                                                            NAME/KEY: CDS
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APPLICANT:
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APPLICANT:
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COUNTRY:
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                                                                              NAME/KEY: (
                                                                 LOCATION:
                    NAME/KEY:
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262 agctaatttttgtanttttagtagagaggggtttcaccatgttgtccaggctggtctn 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 185.8; DB 1;
Pred. No. 1.9e-24;
0; Mismatches 49;
                                                                                                                                                                                                                                                                                       24884-109347
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION NUMBER: US 08/289,221
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
                                       PRIDEN PAPLICATION DAFA:
APPLICATION NUMBER: US 08/348,824
FILING DAFE: 29-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5725 TIGAGCCACCGIGCCCAGCAACC 5747
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                                                                                                                                                                                                                                                         NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.7%;
78.6%;
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EDNESS: double
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Best Local Similarity
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GENERAL INFORMATION: APPLICANT: Stevens, Richard L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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US-07-906-871-15/c
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                                                         61 aaaaaagaccgaccagggctcaaaacaaaaaacctcggaaaagccctggcggtcttttttt 120
                                                                                                                                                                            337 ggtgatccaccgcctcggccccccaaagtactaggattacaggcgtgagccaccgcgtc 396
                                         -----gccaccacgcccagctaa--tttttgtan 276
                                                                                                            277 ttttagtagagacggggtttcaccatgttgtccaggctggtctngaactcctgacctca 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OSAIMS, UNIXO
APPLICANT: OSAIMS, UNIXO
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE. Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891 FILING DATE: 27-DEC-1996 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 188.8; DB 3;
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NAME: NO. 6090620tenburg Ph.D., Carol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE_/DOCKET NUMBER: 24052.419
TELECOMMUNICATION INFORMATION:
TELEPRONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                               Sequence 79, Application US/08781891
Patent No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 39,317
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69.9%;
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nucleic acid
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Yu, Chang-En
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Washington COUNTRY: USA
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                                               gcctcccaagta--
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98104-7092
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APPLICANT: Fu, Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS
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US-08-781-891-79
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US-08-781-891-79
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HEMATOPOIETIC CELL SPECIFIC TRANSCRIPTIONAL REGULATORY ELEMENTS OF SERGLYCIN AND
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                                                                                                                                                                                                                                                                        29990 recordadocrocasarascrassarascrassascrassascrassascrassarrir 30049
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                                                                                                         173 acaatggtcggatctt--ggctcactgcaacctctgcctcccaggttcaagcaattcttc 230
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                                                     29870 TTTGTTTTTTTTTTTTTTTGGGGATAGAGTTCTCACTCTGTCACTAGGCTAGAGT
                                                                                                                                                                                                                       ---gocaccacgcccagctaatttt
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ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 125 Connecticut Avenue, N.W., Suite 300
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,871
FILING_DATE: 19920103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30169 GIGCCIGGCCCAGAGAGAIATTAATGAAAAAAAAA 30206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 gegtecagegeeetggeggtttttaateaagtagaaaa 429
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REFERENCE/POSKET NUMBER: 0627.2830004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)833-7533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/03051
FILING DATE: 13-UL-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/224,035
FILING DATE: 13-UL-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/816,289
FILING DATE: 03 JAN 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/635,544
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                   tgeeteageeteecaagta------
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; Patent No. 5340739
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IOCATION: 24090.25177
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "(translation start:
OTHER INFORMATION: 24110)"
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OTHER INFORMATION: /function= "arsenite resistance
                                                                                                                                                                            NAME/KET: exon
LOCATION: 25524..26009
LOCATION: 25524..26009
LOCATION METHOD: experimental
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /gene= "ACHE"
                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 27005..27274
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 4
                                                                   OTHER INFORMATION: 24110)"

OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 2
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LOCATION: 28008..28129
LIDBNTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /gene= "ACHE"
OTHER INFORMATION: /number= 6
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OTHER INFORMATION: /gene="ACHE"
OTHER INFORMATION: /number= 5
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 3
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 6
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 4
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 5
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OTHER INFORMATION: /number= 2
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IDENTIFICATION METHOD:
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27385..27387
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28129..28131
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LOCATION:
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8322 GATTAFGCCACTGTACTACAGCCTGGGTGACAGAGCAAGACCCTGTCCCTTAAAAAGAAA 8381
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              LOCATION: complement (32569..32628)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 7
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 12
                                                                                                                                                                                                                                                LOCATION: complement (31894..32080)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 9
                                                                                                                                    LOCATION: complement (32386..32468)
OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 8
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 10
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OTHER INFORMATION: /gene= "AR"
OTHER INFORMATION: /number= 14
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); OTHER INFORMATION: /number= 16
US-08-814-095-7
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OTHER INFORMATION: /number= 11
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NAME/KEY: exon
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NAME/KEY: exon
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                                                                               Db 11219 tettettetececetaecetttttttttgagaeagagtettgetetgteaeceaggetgg 11278
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                                      tettittittittittittittittittitgggacagtettgetetgtageccaggetgg 169
    Gaps
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    59; Indels
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Disease and its Use
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APPLICANT: Salbaum, Johannes; Masters, Colin;
APPLICANT: Beyreuther, Konrad
TITLE OF INVENTION: Promoter of the Gene for the
TITLE OF INVENTION: Human Precusor of the Alzheim
TITLE OF INVENTION: Disease and its Use
    0; Mismatches
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MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB
MEDIUM TYPE: storage
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/325,745
FILING DATE: 19-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,546
FILING DATE: 16-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,330
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/385,758
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APPLICATION NUMBER: US/08/483,488
FILING DATE: 07-UN-1995
CLASSIFICATION: 536
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14-AUG-1989
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APPLICATION NUMBER: UK 8820450.8
APPLICATION NUMBER: 30-aug-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08483488
Patent No. 5853985
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    Matches 266; Conservative
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OPERATING SYSTEM:
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APPLICANT: BUNDEG, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN
CURRENT APPLICATION NUMBER: US/09/385,982
CORRENT FILING DATE: 1999-08-30
EARLIER PILING DATE: 1999-06-30
EARLIER PILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER PILING DATE: 1998-01-27
WUMBER OF SEQ ID NOS: 544
                                                                                                                                                                                                                                                                                                                                                                             Score 189.4; DB 2;
Pred. No. 4.3e-25;
0; Mismatches 43;
                                              MTI 212.6-KGB
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OTHER INFORMATION: n = A,T,C or G
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: WT.
TELECOMMUNICATION INFORMATION:
                                                                                             TELEPHONE: (914) 332-1700 TELEFAX: (914) 332-1844
                                                                                                                                                                                                                                                                                                                                                                                  16.0%;
79.7%;
                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 3804 base pairs
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Best Local Similarity 79.7
Matches 243; Conservative
                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-483-488-5
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us-09-963-333-7.rni

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                                            agtagaaaagctgcattataccacttgcttcngttgcnttcagtgagaacgaagaaatgg
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APPLICANT: Dean, Nicholas M.
TITLE OF INVENTION: OF HOMAN THYMIDYLATE SYNTHASE EXPRESSION
TITLE OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
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Patent No. 6087489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 297.8; DB 3;
Pred. No. 6.4e-44;
0; Mismatches 2;
                                                                                                                                      ISPH-0309
                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/089,195
FILING DATE: herewith
          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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) Sequence 42, Application US/09608285A

) Patent No. 6335013

) GENERAL INFORMATION:
                                                                                                                                 REPERENCE/DOCKET NUMBER: ISP
TELECOMMUNICATION INFORMATION:
TELEPRONE: (609) 810-1315
TELEFAX: (609) 810-1454
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                         REGISTRATION NUMBER: 32,257
                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res
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                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Jane Massey Licata
Floppy disk
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Best Local Similarity 99.3
Matches 299; Conservative
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                                                                                                                                                                                                                                        Single
                                                                                                                                                                                                                                                                             Takeishi,K.
                                                                                                                                                                                                                                                                                        Kaneda,S.
Ayusawa,D.
Shimizu,K.
                                                                                                                                                                                                                           Nucleic Acid
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PAGES: 2035-2043
DATE: 25-MAR-1985
                                                                                                                                                                                                                                                   Unknown
                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                             JOURNAL: 1
                                                                                                                                                                                                                                                                                                                AUTHORS:
AUTHORS:
AUTHORS:
                                    SOFTWARE:
                                                                                                                                                                                                                                                                                          AUTHORS:
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                                                                                                                                                                                                                                                                              AUTHORS
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APPLICANT: Ford, John

Search completed: July 26, 2002, 16:37:26 Job time: 24120 sec

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QY Db	QY Db	QY	Qy Db	QY	QY	OY Db	QY	QY	Qy Db	QY Db	QY	RES AXC LOC DEF ACC VEF KEY	REF A	FEP BAS ORI

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PAT 09-JAN-2
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Cancer gene determination and therapeutic screening using signat
                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                807 gtacatgattgcgcacatcacgggcctgaagccaggtgactttatacacactttgggaga 866
                                                                                                867 tgcacatatttacctgaatcacatcgagccactgaaaattcagcttcagcgagaacccag 926
  Length 18596;
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                          Indels
Score 613.2; DB 6;
Pred. No. 9.8e-117;
0; Mismatches 63;
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MEDLINE 95226450 Location/Qualifiers 11598 Acranism="Rattus norvegicus" Source Ab. xref="taxon:10116" Cell_line="H35" Cell_line="H35" Cell_line="H35" Cell_line="dimer: putative" Aproduct="dimer: putative" Codon_start=1 Aproduct="thymidylate synthase" Aproduct="thymidylate synthase	Query Match 45.4%; Score 697.8; DB 10; Length 1598; Best Local Similarity 87.7%; Pred. No. 2.4e-134; 0.2.4e-134; 0.3.2.4e-134; 0.	241 aggaaggacgaccgaaccggaaccggtattcggtattcggatgactacacctacacctacgaatgaaggacgctaccctaccgaatliliiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii	Oy 381 gasgaqtusctytogttattatcaagggatccacaagtgtaaagggttcttccaaggga 420	Db 358 CGACAGGAAGCAGCCCAGGTTATGGATTCCAGTGCGAGCAGTCTTTTGGAGCAGAC 417 Oy 541 tacagagatatggaatcagattattcaggacaggagttgaccaactgcaaagggtgatt 600 Db 418 TACAAAGATATGGATTCAGATTATCGGGTCAAGGAGCAGCCGAAAAAGTGATT 477 Oy 601 gacaccatcaaaaccaaccctgacgacagaagaatcatcatgtgcgcttggaatccaaga 660 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
219 365 279 279 425 339 485 399 605 519 665	725 639 785 699	agccaggtga 845 AGCCAGGTGA 759 cactgaaat 905 	asgitigagaa 955 AAGTIGAGAC 879 Atccaectat 1025 ATCCAACGAT 939	D) Dp mRNA linear ROD 30-MAY-2000 Dise synthase mRNA, complete cds. Display to the complete cds.	urognathi; Muridae; Murinae; urognathi; Muridae; Murinae; S., Reston,J.T., Maley,G.F. and hymidylate synthase cDNA: n and mouse thymidylate synthases
160 GGAGGACCGCACGGCACTGGCACCCTGTCGGTTTCGGCATGCAGGCACGATACAGCCT 306 gagagatgaattccctctgctgacaaccaaacgtgtgttctggaagggtgttttggagga 220 [all]		786 egocagotacgocotgotcacgtacatgattgcgcacatcacgggcctgaagccaggtga 	11111 1	960 159E ymidylat	L ON EN

452 705 498 558

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986 bp mRNA linear ROD 22-JAN-2
Mus musculus, clone MGC:28246 IMAGE:3994204, mRNA, complete cds.
BC020139
MCC.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M
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Submitted (19-DEC-2001) National Institutes of Health, Mammaliar
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X., Hulyk, S.W., Hale, S.M.,
S., Martin, R.G., Muzny, D.M.
                                                                                                     ttetatgtggtgaacagtgagetgteetgecagetgtaccagagatcgggagacatggge 765
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                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: ogapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                     946 attottogaaaagttgagaaaattgatgacttcaaagctgaagactttcagattgaaggg
                                  886 cacatogagocactgaaaattcagottcagogagaacccagacctttcccaaagctcagg
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Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
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Strausberg, R.
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COMMENT
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VRKDDRTGTGTLSVFGMQARYSLRDEFPLLTTKRVFWKGVLEELLWFIKGSTNAKELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKGVKIWDANGSRDFLDÖLGFSTREBGDLGPVYGFQWRHFGAEYRDMESDLPLMALPP
CHALCQFYVVNSELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITGLKPGDFIHTL
GDAHIYLNHIEPLKIQLQREPRPFPKLRILRKVEKIDDFKAEDFQIEGYNPHPTIKME
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                                                                                                                                                                                                                                                       "Jobe" Tall alternative splicing variant The protein encoded by this gene is 34aa shorter than the full-length isoform. This variant uses an alternative splice site resulting in it lacking 102nt in the coding region compared to the full-length isoform reported in Acc#
Molecular biology and Cytogenetics; 5-6-50 Shin-machi, Hino, Tokyo 191-0002, Japan (E-mail:hisatomi@srl.srl-inc.co.jp, Tel:81426483793(ex.7926), Fax:81426484043)
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Pred. No. 1.2e-140;
0; Mismatches 0; Indels 102;
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/product="thymidylate synthase"
/protein.id="BAB88677.1"
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                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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/cell_line="KATO III"
                                                     Location/Qualifiers
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                                                                                                                              /chromosome="18"
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89.2%;
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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                         BC013919

Homo sapiens, Similar to thymidylate synthetase, clone MGC:22884
IMAGE:4048625, mRNA, complete cds.
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VRKDDRTGTGILSVFGMQARYSLRDEFPLLTTRRVFWKGVLEELLWFIKGSTNAKELS
SKGVKIWDANGSRDFLDSLGFSTREEGDLGPVYGFQWRHFGAEYRDMESDYSGQGVDQ
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MGLGYPFNLASYALLTYMTAHIGGLRPGDFIHTLGDAHIYLNHIEPLKIQLQREPRPF
PKLRILRKVEKIDDPRAEDFQLSCYRPPTIKMEMAV"
PKLRILRKVEKIDDPRAEDFQLSCYRPPTIKMEMAV"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1569)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadanesystemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
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/db_xref="taxon:9606"
/clone="MGC:22884 IMAGE:4048625"
/tlssue_trype="Bone marrow, chronic myelogenous leukemia"
/clone_lib="NIH_MGC_54"
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Submitted (OT SEP-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                  1381 TAGAATATTTTAAGAATTTCACAAGCTATTCCCTCAAATCTGAGGGAGCTGAGTAACACC
/product="Similar to thymidylate synthetase" /protein_id="AAH13919.1"
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Contact: MGC help desk
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96. .1037
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                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgi.nih.gov
ShevChenko,r, wetherby,K.D. Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Ilim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., WcCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Thongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 4 Row: p Column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRKDDRTGTGTLSVFGMQARYSLRDEFPLLTTRRVFWRGVLEELLWFIRGSTNAKELS
SKGVKIWDANGSRDFLDSLGFSTREEGDLGPVYGFQWRHFGAEYRDMESDYSGQGVDQ
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MGLGVPFNIASYALLIYMIAHITGLKPGDFIHTLGDAHIYLNHIEPLKIQLQREPRPF
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                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 153)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507750.
                                                                                         Direct Submission
Submitted (OS-FEB-201) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ccgccgccatgcctqtggccggctcggaqctgccgcgcggcccttgcccccgccgc 155
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                                                                                                                                                                                                                                     cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone_lib="NIH_MGC_21"
/lab_host="DH10B-R"
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359 c 389 g 376 t
                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Pred. No. 7.7e-300;
0; Mismatches 3;
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/db_xref="taxon:9606"
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78. .1019
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Db 1021 ACTATTABAATGGABATGGCTGTTTAGGGTGCTTTCAAAGGAGGTTGTAGG 1080 Qy 1081 gtctttaggggttgggttggctgggtgaaagttcttttggtcttaaaagaagaagag 1140 Db 1081 GTCTTTAGGGGTTGGGGTGGAGGTAAAAGTTCTTTTTGCTCTAAAAGAAAAGG 1140 Qy 1141 aactaggtcaaaatctgtccgtgacctatcagttattaatttttaaggatgttgcact 1200 Db 1141 AACTAGGTCAAAATCTGTCCGTGACCTATCAGTTATTTAAGGTGTGCCACT 1200 Qy 1201 ggcaaatgtgaactgtgccgttctttccataataaaaggctttgagttaactcactgagg 1260 Qy 1261 gtatctgacaatgctgggttatgaacaaagtgaggagatgaatgtaactcactgagg 1260 Qy 1261 gtatctgacaatgctggggttatgacaaaagtgaggagaatgaat	RESULT 2 HOUSEN LOCUES ACCESSION MO20308.1 G1:37478 KERTON WERSTON WERSTON WERSTON WERSTON MARINATION Homen mRNA for thymidylate synthase (EC 2.1.1.45). WERSTON WERSTON MARINATOR: A Wetacoa: Chordata; Craniata; Vertebrata; Euteleoston: Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston: Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. MERTANDEN REFERENCE ONGANISM REFERENCE AUTILE MUCLOCITICA SOUNCAL JOBASS 1 to 1536) AUTILE SUNCHAL JOBASS 1 to 1536) AUTILE MUCLOCITICA SOUNCAL JOBASS 1 to 1536) MEDLINE JOURNAL MUCLOCITICA SOUNCAL JOURNAL MUCLOCITICA SOUNCAL JORGATION CONTINE MEDLINE JORGATION CONTINE JORGATION CONTINE LOCATION CONTINE ADAI MICHAEL AND SEPTION JORGATION CONTINE MISC_feature JOCUT 103 MOSTON CONTINE ADAI MICHAEL AND SEPTION MISC_feature JORGATION CONTINE MISC_feature JORGATION MISC_FEATURE JORGATI
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/tissue_type="neuroblastoma cells"
/tissue_type="neuroblastoma cells"
/lab_host="DH108"
/note="Organ: Drain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library is not normalized, but is the control for
the normalized libraries. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies,
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
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Homo sapiens cDNA clone CS0DA001YD20 3
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                          gggagacatgggcctcggtgtgcctttcaacatcgccagctacgccctgctcacgtacat
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tgccctctgccagttctatgtggtgaacagtgagctgtcctgccagctgtaccagagatc
                                                                                                                                                                                                813 gattgcgcacatcacgggcctgaagccaggtgactttatacacac--tttgggagatgca
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Catarrhini; Hominidae;
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Li,W.B., Gruber.C., Jessee,J. and Polayes,D.
Frull-length cDNA libraries and normalization
Unpublished (2001)
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/db_xref="taxon:9606"
/clone="CSODA001XD20"
/clone_lib="LTI_NFL011_NBC1"
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web
Location/Qualifiers
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Mammalia; Eutheria; Primates;
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AL515910 LTI_NFL011_NBC1
prime, mRNA sequence.
AL515910
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1168 1228 aagtgagägaatgaatgtatgtgctcttagcaaaaacatgtatgtgcattcaatcc 1348 ttttaagaatttoacaagctattooctoaatotgaggagotgagtaaoacoatcgato 1468 actttcagattgaagggtacaatccgcatccaactattaaaatggaaatggctgtttagg 1048 $\mathfrak{gtgotttcaaaagaagctCgaaagatattgtcagtctttaggggttggggctggatgccgag}$ 1108 324 748 868 928 444 384 628 688 804 744 808 684 624 564 504 TITIAAGAAITICACAAGCIAITCCCICAAAICIGAGGGAGCIGAGINACACCAICGAIC 24 Gaps cacatatttacctgaatcacatcgagccactgaaaattcagcttcagcgagaacccagac 863 GAAGAATCWIMAIGIGGGCTIGGAATCCAAGAGNICIYCCICIGAIGGSGCIGCCICCAI acatgattgcgcacatcacgggcctgaagccaggtgactttatacacactttgggagatg ctttcccaaagctcaggattcttcgaaaagttgagaaaattgatgacttcaaagctgaag gtaaaagttctttttgctctaaaagaaGaaggaactaggtcaaaaatctgtccgtgacct ; others Length Indels 디 fliang@lifetech.com URL : http://fulllength.invitrogen.com" 1 206 c 188 g 269 t 11 57.8%; Score 888.4; DB 9; 97.5%; Pred. No. 1.7e-189; ive 10; Mismatches 12; atgatgtagagtgtggttatgaa 1491 23 ATGATGTAGAGTGTGGTTATGAA 1 Matches 900; Conservative

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Homo sapiens
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17 a 265 c 250 g 192 t 8 others
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BP 191 91006 EVRT cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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                                                                                                                                                                  /tissue_type="neuroblastoma cells"
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                                                                                                                                                    /sex="male"
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was primed with a Not1-oligo(dT) primer. Five prime enemriched, double-stranded cDNA was digested with Not I cloned into the Not I and Eco RV sites of the pCMYSPORT vector. Library was normalized. Library was constructed Life Technologies. Context: Fend Liang Life Technologie a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com.?
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Li,W.B., Gruber,C., Jessee,J. and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Pred. No. 5.7e-192;
1; Mismatches 2;
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/tissue_type="placenta"
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Location/Qualifiers
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/clone="CSODIO61YF09"
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99.7%;
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Homo sapiens CDNA clone CSODA001YD20 5
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 995)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 gcacgggcaccggcacctgtcggtattcggcatgcaggcgcgctacagcctgagagatg
                                        314 aattooototgotgacaaccaaacgtgtgttootggaagggtgttttggaggagttgotgt
                                                  ggtttatcaagggatccacaaatgctaaagagctgtcttccaagggagtgaaatctggg
                                                                                             GGTTTATCAAGGGATCCACAAATGCTAAAGAGCTGTCTTCCAAGGGAGTGAAAATCTGGG
                                                                                                                          atgccaatggatcccgagactttttggacagcctgggattctccaccagagaagaagggg
                                                                                                                                    acttgggcccagtttatggcttccagtggaggcattttgggggcagaatacagagatatgg
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AL515911 LTI_NFL011_NBC1
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AL515911
AL515911.1 GI:12779404
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/note-"Organ: brain, Vector: pCMVSPORT 6; 1st strand cl
was primed with a NotI-oligo(dT) primer. Five prime encerriched, double-stranded cDNA was digested with Not I
cloned into the Not I and Eco RV sites of the pCMVSPORY
vector. Library is not normalized, but is the control
the normalized libraries. Library was constructed by Li
Technologies. Contact: Feng Liang Life Technologies,
division of Invitrogen 9800 Medical Center Drive Rockvi
, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
fliang@lifetech.com URL:
http://tullength.invitrogen.com"
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                                                                                                                                                                                                                                                                                                    60.2%;
98.1%;
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Db 84		DD 301 TCAAGGGAICCACAAAIGCTAAAGAGCIGICTTCCAAGGGAGTTAAAATCIGGGAIGCCA 360
Oy 1488 Db 24	88 tgaactttaAagttgttttatatg 1511 	OY 440 atgratecegagaetttttggaeageetgggatteteeeeagagaaagaggaettgg 499
RESULT 6 AL513730 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AL513730 AL513730 1.T_NFL006_PL2 Homo sapiens cDNA clone CL0B prime, mRNA sequence. AL513730 AL513730.1 G1:12777224 EST. human. Homo sapiens	
REFERENCE AUTHORS TITLE JOURNAL COMMENT	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 978) 1i, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 ENRY cedex - France	
FEATURES Source		Qy 800 tgctcacgtacatgattgcgcacatcacgggcctgaagccaggtgactttatacacactt 859
		OY 860 t-gggagatgcacatatttacctgaatcacatcgagccactgaaaattcagcttcagcga 918
BASE COUNT ORIGIN	23	
Query Best Match 1	Similarity 98.6%; Pred. No. 6.2e-200; Length 978;	RESULT 7 AL542409 LOCUS LOCUS DEFINITION AL542409 LTI_FL002_PL1 Homo sapiens CDNA clone CSODE010YH04 5 p ACCESSION AL542409 LTI_FL002_PL1 Homo sapiens CDNA clone CSODE010YH04 5 p ACCESSION AL542409.1 GI:12874425 KEYWORDS FOUR SOURCE HOMO sapiens BURATYOLS: Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. REFERENCE I (Dases 1 to 935) AUTHORS Li,W.B., Gruber, C., Jessee, J. and Polayes, D.
DD 121 QY 260 DD 181 QY 320 QY 320 QY 380	121 AGTACCTGGGGGCACACACACACACACACACACACGGGGGGGG	THIL-LENGTH COUNTY Unpublished (2001) Contact: Genoscope Genoscope - Centre National de Sequencage BP 1919 19106 EVRY cedex - France Rmail: seqreféqenoscope.cns.fr, Web : www. Location/Qualifiers 1. 935 /organism="Homo sapiens" /db_xref="texon:9606" /clone="CSODE010YH04"

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AL547612 AL547612 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1008YH21 5

DEFINITION

RESULT ALS47612 LOCUS

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was primed with a NotI-oligo(dT) primer. Five prime en
enriched, double-stranded cDNA was digested with Not I
cloned into the Not I and Eco Ry sites of the pcWNSPORT
vector. Library was normalized. Library was constructed
Life Technologies. Contact: Feng Library was constructed
Life Technologies. Contact: Feng Library was constructed
Life Technologies. Contact: Feng Library was Constructed
Life Technologies. Contact: English Life Technologi
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email : fliang@lifetech.com URL :
http://tullength.nnvitrogen.com"
http://tullength.nnvitrogen.com"
                                                                                    Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. Li, W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length DNA libraries and normalization Onpublished (2001) Contact: Genoscope Cente National de Sequencage Genoscope - Centre National de Sequencage BPP 191 91006 EVRY cedex - France Email: segrefégenoscope.ons.fr, Web : www.genoscope.cns.fr.
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Pred. No. 1.2e-218;
1; Mismatches 1;
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99.8%;
prime, mRNA sequence.
AL547612
AL547612.1 GI:128818
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10835001 This clone has the following problem: no 5' EST match. Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:3141419"
/tissue_type="Ovary, adenocarcinoma"
/clone_lib="NIH_MGC_9"
/lab_host="DH10B-R"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                     gaaGaaggaactaggtcaaaaatctgtccgtgacctatcagttattaattttaaggatg
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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The present invention describes colon tumour associated proteins (I) and (II) and (II) can be used in gene therapy and vaccine production. (I) and (II) and be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the actifying mutations or deletions in a patient's genome that affect the actifying mutations of them. Additionally, (II) may be used to patients own production of them. Additionally, (II) may be used to patients own production of them. Additionally, (II) may be used to complementary sequences may also be used as DNA probes in diagnostic polymerase chair reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and in assays to identify modulators of TCAP expression and activity. The anti-(I) antibodies and antagonists may also be used to down regulate as diagnostic agents for detecting the presence of TCAP expression and activity. The anti-(I) antibodies and antagonists may also be used to down regulate as diagnostic agents for detecting the presence of TCAPs in samples and antagonists may also be used to down regulate as diagnostic agents for detecting the presence of TCAPs in samples and AMX2451 represent nucleotide and amino acid sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secrist H, Benson DR, Meagher MJ, Stolk JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colon tumor associated proteins and nucleic acids useful for the
immunogenic; gene therapy; vaccine; colonic cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prevention, diagnosis and treatment of colonic cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 254; 472pp; English.
                                                                                                                                                                                                                                            10-JAN-2000; 2000US-0480321.
11-FEB-2000; 2000US-054629
06-MAR-2000; 2000US-0519444.
19-MAY-2000; 2000US-0572251.
29-JUN-2000; 2000US-0609448.
                                                                                                                                                                            29-DEC-2000; 2000WO-US35596.
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                                                                                    WO200149716-A2.
                                            Homo sapiens.
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                                                           9;
                                  Length 2966;
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Sequence 2966 BP; 808 A; 640 C; 664 G; 854 T; 0 other;
                                 Score 383.8; DB 23;
Pred. No. 7e-90;
0; Mismatches 292;
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ID ABL05761 standard; cDNA; 966
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AC ABL05761;
                                  25.0%;
65.9%;
                                                           Matches 575; Conservative
                                               Similarity
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPM at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolated nucleic acid detection reagent for detecting 1000 or mores from Drosophila and for elucidating cell signalling and cell-cel.
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                                                       Drosophila melanogaster expressed polynucleotide SEQ ID NO 11765.
                                                                                                                      developmental biology; cell signalling; insecticide;
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Pred. No. 4.5e-89;
0; Mismatches 287;
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Best Local Similarity 66.0%;
Matches 568; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US09231.
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2000US-0614150.
(first entry)
                                                                                                                                                                   pharmaceutical; gene; ss
                                                                                                                                                                                                                                  Drosophila melanogaster,
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/product= macrophage inflammatory protein II complement (27137..27424) /product= interferon regulatory factor 1 28661..29741

/product= protein T1.1 complement (58976..60175)

..29741

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/product= glycoprotein M complement (69412..69915)

/product= glycoprotein L complement (88410..88910)

/*tag≃

/product complement-binding protein

..11236

/*tag≈

/*tag≈ a

Location/Qualifiers

/product= glycoprotein B complement (17261..17875)

O

/product= interleukin 6 complement (21548..21832)

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Key
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20843 AGGTATAGTCTGCGGGACCACTTTCCCTTACTAACCACAAAGCGGGTGTTTTGGCGAGGC 20784
                                                          20783 GTAGIGCAAGAGCIGCTITGGITTCIGAAGGGGAGTACTGACTCCAGGGAGCTITCAAGA 20724
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                                                                             415 aagggagtgaaaatctgggatgccaatggatcccgagactttttggacagcctgggattc 474
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     295 cgctacagcctgagaatgaattccctctgctgacaaccaaacgtgtgttctggaagggt 354
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/product= interferon regulatory factor 2 89600..90541 'product interferon regulatory factor 3 /product= interferon regulatory factor 4

/product= glycoprotein X complement (93636..94127)

90173..90643

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New nucleic acid encoding Kaposi's sarcoma associated herpes virus proteins - useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bohenzky RA, Chang Y, Edelman IS, Moore PS, Russo JJ;
                                                                                                     /product= immediate early protein
                                         /product= capsid protein IV
                                                            complement (123808..127296)
complement (111931..112443)
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96US-0686349.
96US-0686350.
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96US-0708678.
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                                                                                                                                                 WO9804576-A1.
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25-JUL-1996;
25-JUL-1996;
25-JUL-1996;
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                                                              CDS
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interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis; complement-binding protein; glycoprotein; capsid protein IV; infection; immediate early protein; Kaposi's sarcoms; protective vaccine; lymphoma; lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides; HIV immune status; anti-inflammatory agent; therapy; ds.

Kaposi's sarcoma-associated herpes virus.

KSHV; HHV8; human herpes virus 8; macrophage inflammatory protein II;

KSHV long unique coding region and terminal repeat.

03-AUG-1998 (first entry)

AAV19941;

AAV19941 standard; DNA; 137507 BP

847 tttatacacactttgggagatgcacatatttacctgaatcacatcgagccactgaaaatt 906

cagetteagegagacecagacettteecaaageteaggattettegaaaagttgagaaa 966

907

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20797 GAGATGGAGATGGCCGTTT 20779 1027 aaaatggaaatggctgttt 1045.

967 attgatgacttcaaagctgaagactttcagattgaagggtacaatccgcatccaactatt 1026

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claims the judiciant residual control of the proteins of the ground sequence, and response in the proteins of the ground sequence. The present invention also specifically claims the individual open reading frame (ORF) nucleotide sequences from the ground which encode the individual proteins, but these sequences are not given. A non-human animal infected with RRV can be used for testing the efficacy of drug in the treatment of condition associated with infection with RRV such as Kaposi's sarcoma, lymphoprolificataive disorders, B-cell hyperplasia, lymphadenopathy, splenomegaly, hyperplasia, lymphadenopathy, splenomegaly, hypergammaglobinulinaemia or autoimmune heamolytic anaemia, by administering the drug to a immuno-compromised non-human primate preferably Rhesus macaque monkey obtained by as a result of infection by Sinian Immunodeficiency Vitus (STV). RRV is useful for producing associated with RRV infection. It is also useful for testing the efficacy of the candidate vaccine against RRV infection or conditions associated with its infection with RRV infection or conditions cubject capable of infection with RRV, incoulating the subject with RRV and observing the effect of vaccine, administering the subject with RRV and observing the effect of vaccine, administering the subject and Abb53205 to AAB53213 represent sequence used in the exemplification of the
macaca mulatta rhadinovirus 17577 (RRV). AAC64754 represents the
                                 genome sequence, and AAB53123 to AAB53204 represent the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention.
8888888888888888888888888888888
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Sequence 133719 BP; 32746 A; 35648 C; 34521 G; 30804 T; 0 other;

DL-B; thymidylate synthase; dihydrofolate reductase; probe; HHV-8; Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein; Raposi's sarcoma; beta-chemokine-like; hydridisation; vIL-6; ss.

Kaposi's sarcoma associated herpesvirus.

Synthetic

DL-B; Bcl-2

WO9804284-A1.

Human herpesvirus 8 (HHV-8) divergent locus DL-B probe 1.

(first entry)

15-JUL-1998

AAV10240;

BP.

AAV10240 standard; DNA; 1014

RESULT AAV10240

0; 21637 CACGGCGAGCTGCAGTACTTGGCGCACCTGGATTTAATTATTAAACACGGCGTGCAGAGG 21578 187 cacggggagctgcagtacctgggggcagatccaacacatcctccgctgcggcgtcaggaag 246 ttgctgtggtttatcaagggatccacaaatgctaaagagctgtcttccaagggagtgaaa 426 atctgggatgccaatggatcccgagactttttggacagcctgggattctccaccagagaa 486 Gaps agagatgaattccctctgctgacaaccaaacgtgtgttctggaagggtgttttggaggag gacgaccgcaccggcaccggcacctgtcggtattcggcatgcaggcgcgctacagcctg Score 404.6; DB 21; Length 133719; 0 Indels Pred. No. 1.7e-94; 0; Mismatches 284; 26.3%; 66.9%; Best Local Similarity 66.9 Matches 575; Conservative Query Match 247 307 21517 367 21457 427 δŽ δ ŎΣ d QΥ δž

macrophage inhibitory protein (VMIP) 1A and -1B and beta-chemokine-like (BCK) protein. The sequences of these proteins are given in AAM40100-W40108. The invention claims the mentioned proteins and a polynucleotide containing HHV-8 genes encoding one or more of these proteins. The invention also claims that the polynucleotide and the proteins may be used directly or indirectly, e.g. using antibodies to the proteins, to diagnose an HHV-8 associated disease, e.g. Kaposi's The present probe was synthesised for detecting human herpesvirus-8 (HHV-8) divergent locus DL-B which lies between open reading frames I1 and 17. Sequencing of the HHV-8 divergent locus DL-B revealed the presence of nine viral ORFs with gene products related to cellular proteins. These proteins include the thymidylate synthase (TS), dihydrofolate reductase (DHFR), Bcl-2 homologue, IE-1A, IE-IB and, four cytokines which include viral interleukin-6 (vIL-6), viral sarcoma, Castleman's disease, multiple myeloma and body cavity based large cell lymphoma (BCBL). The proteins have also been claimed to be New human herpes virus gene region containing 8 open reading frames - useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based Hardwick JM, Hayward GS, Nicholas J, Reitz MR; Claim 4; Pages 51-52; 84pp; English. 97WO-US12931. 96US-0022591. (UYJO) UNIV JOHNS HOPKINS WPI; 1998-130422/12. large cell lymphoma 24-JUL-1997; 25-JUL-1996; 05-FEB-1998.

Sequence 1014 BP; 216 A; 239 C; 286 G; 273 T; 0 other;

compounds for drugs to treat HHV-8 diseases.

useful in screening

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11097 CTGTCCTGCCAGCTGTACCAGAGGTCCGCCGACATGGGCCTCGGGGTCCCGTTTAACATC 21038
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21397 ATTTGGGACGCGCACGGGTCCCGCGCCTTTTTGGCGGCGCGCAGGGCTTCGGGGACCGCCGC 21338
                                                                                                   21337 GAGGGCGATCTGGGGCCGGTGTACGGCTTCCAGTGGACACATTTTGGGGCGGAGTACAGG 21278
                                                                                                                                                                                                      21277 GGGCCCGACGCCAACTACGAGGGTCAGGGGGTGGACCAGCTGCGTTACGTGGTGGATCTA 21218
                                                                                                                                                                                                                                                                                                            21217 ATTAACAGGCGCCCCACGATCGCCATCGTTATGTGCGCGTGGAACCCCGCGGACCTC 21158
                                                                                                                                                                                                                                                                                                                                                                                                                21157 GCGCGGATGGCTCTCCTTGTCACGTTTTGTGTCAGTTTTACGTGGCTCGGGGGGAG 21098
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                                                        gaaggggacttgggcccagtttatggcttccagtggaggcattttgggggcagaatacaga 546
                                                                                                                                                           gatatggaatcagattattcaggacagggagttgaccaactgcaaagagtgattgacacc
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The present sequence represents the nucleotide sequence of Varicella virus, Dumas strain. The specification describes a method for the quality control of an attenuated pox vaccine, characterised in that the DNA sequence of specific parts of the viral genome in a sample is determined and proved to be conserved rather than mutated in comparison
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actgtgccagttctttccataataaaggctttgagttaactcactgagggtatctgaca
                                                                                            tatgtgcatttcaatcccacgtacttataaagaaggttggtgaatttcacaagctatttt
                                                                                                                                          tgagtaacaccatcgatcatgatgtagagtgtggttatgaactttaAagttgttttatat
                                                                                                                                                                                                                                     Dumas strain; pox vaccine; vaccine; poxvirus disease; chickenpox;
                                                           241 actgtgccagttctttccataataaaaggctttgagttaactcactgagggtatctgaca
                                                                                  Sequence 124884 BP; 33789 A; 29295 C; 28177 G; 33623 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of the Varicella virus Dumas strain
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Score 408; DB 22;
Pred. No. 2.1e-95;
0; Mismatches 295;
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66.5%;
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                          Conservative
               Similarity
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    Query Match
Best Local Simi
Matches 585;
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AC AAH7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; schizophrenia; developmental disorder; spina bifida cystica; Tourette's syndrome; bipolar illness; autism; conduct disorder; attention deficit disorder; obsessive compulsive disorder; chronic multiple tic syndrome; learning disorder; polymorphism; ds.
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Note: the present sequence is not shown in the specification, but was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assaying method, useful for prognosis and diagnosis of disease, comprises contacting sample with a mutant analyte-binding enzyme and detecting binding -
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                                                              sequences that are differentially expressed during foam cell differentiation. The polynuclectide sequences of the invention or a composition comprising these polynuclectides are useful as a high throughput method for detecting altered expression of one or more polynuclectides in a sample. The polynuclectides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynuclectide sequences can also be used as PCR primars and probes. The polynuclectide sequences can also be used useful in gene therapy. Ass39401e Ass39621 represent the human polynuclectide sequences of the invention are also polynuclectide sequences of the invention which are differentially
                                                    numan polynucleotide
foam cell
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                                                    present invention relates to the isolation of human
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are differentially expressed in foam cell development
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WO200175067-A2

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GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvir
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
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STREET: One Liberty Place, 46th floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48.6; DB 4; Length 1292;
Pred. No. 0.002;
0; Mismatches 84; Indels 0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,568A
FILING DATE: 02-UNR-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
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WEDING TYPE: FLOPPY disk
COMPUTER: TRM PC COMPUTED:
OPERATING SISTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08458568A Patent No. 5821339
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ATTONEYAGENT INFORMATION:
NAME: Leary Ph.D., Kethryn R.
REGISTRATION NUMBER: 36,317
                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
         TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 37
SEQUENCE CHARACTERISTICS:
LENGTH: 1292 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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TELEPAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 702 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.28
Best Local Similarity 54.13
Matches 99; Conservative
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COUNTRY: US
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-458-568A-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-283-471A-37
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APPLICANT: Chou, Joany
TITLE OF INVENTION: Method For Treating Tumorigenic Diseases
TUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48.6; DB 4; Length 1292;
Pred. No. 0.002;
0; Mismatches 84; Indels 0
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APPLICATION NUMBER: US/09/283,471A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Zeller, James P.
REGISTRATION NUMBER: 28,491
REFERENCE/DOCKET NUMBER: 27373/32742A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
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COUNTRY: United States of America
ZIP: 6066-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS MS-DOS
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CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 37, Application US/09283471A Patent No. 6340673 GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/419,853
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                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA (genomic)
US-08-483-533-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.2%;
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEG ID NO: 3
SEQUENCE CHARACTERICS:
LENGTH: 1292 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 11-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.15
Matches 99; Conservative
                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: (
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1608 TATTCAAATCATATTGATGCGATKCGMAACACCATTAGCACGTGAAAGCTTCAATCCTCC 1549
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                                                                    877 tacctgaatcacatcgagccactgaaaattcagcttcagcgagaacccagacctttccca 936
                                                                                                                                                           937 aageteaggattettegaaaagttgagaaaattgatgaetteaaagetgaagaettt-ea 995
                                                                                                                                                                                                                                                                              1490 AATTGTTGACTATGAATCACATCCAGCMATAAAAGCTCCMATAGCAKTGTAG 1439
                                                                                                                                                                                                                                                    996 gattgaagggtacaatccgcatccaactattaaaatggaaatggctgtttag 1047
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TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard 4.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/714,918
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09266417 Patent No. 6228588
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee, Ving J.
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. D
SOTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/26
FILING DATE: March 9, 1999
CLASSIFICATION: 435
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EDNESS: single
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ADDRESSEE: Lyon & Ly
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STATE: California
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US-09-266-417-7
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APPLICANT:
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APPLICANT:
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1908 TIGATCAACTTAAAACAGTAATTGAACAAATTAAGCATAATCCAGATTCAAGGCGACACA 1849
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                                                                                                                                                                                             teatgigegetiggaatecaagagatetteetetgaiggegetgeeteeatgeea 697
                                                                                                                                                                                                                                                                                           tetgecagitetatgiggigaacagigagetgiecigecagetgiaceagagaicggagg 757
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                                                                                             758 acatgggcctcggtgtgcctttcaacatcgccagctacgccctgctcacgtacatgattg
Score 121.2; DB 4; Length 3479; Pred. No. 1.7e-22;
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STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Method for Treating Tumorigenic TITLE OF INVENTION: Diseases NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPACTORS
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/483,533
PTITING DATE: 07-MAR-95
                                                  6; Mismatches 194;
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REFERENCE/DOCKET NUMBER: 28097/32742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: CLILUST, STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC PC-DOS/MS-DOS
COMPATIBLE SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/419,853
FILING DATE: 11-APR-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08483533 Patent No. 6172047
     7.9%;
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  Query Match
Best Local Similarity 56.8
Matches 268; Conservative
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PRIOR APPLICATION DATA:
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CITY: Chicago
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                                                                                                                                                                    20243 CCACTACGGCTGCAGCTGACGCGCACTCCACGTCCTTTCCGCGCCTGGAGATACTCCGG 20184
                                                                                       20183 ICTGTTTCCTTCCATGGAAGAGTTTACACCTGATGATTTTAGACTGGTGGACTACTGCCCG 20124
                                                                      715 gigaacagigagcigiccigccagcigiaccagagaicgggagacaigggccicggigig 774
                                                                                                                                                                                                                    894
895 ccactgaaaattcagcttcagcgagaacccagacctttcccaaagctcaggattcttcga
                                                                                                                                               octttcaacatcgccagctacgccctgctcacgtacatgattgcgcacatcacgggcctg
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TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                               20123 CATCCTACCATTCGTATGGAAATGGCAGTATAG 20091
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
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APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: September 15, 1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: December 22, 1995 APPLICATION NUMBER: 60/003,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08714918 Patent No. 6037123
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Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
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(213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3
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APPLICANT: Benton, Bret
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STATE: California
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CLASSIFICATION:
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APPLICANT:
APPLICANT:
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1908 TIGATCAACTIAAAACAGIAATIGAACAAATTAAGCATAATCCAGATTCAAGGCGACACA 1849
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                                                                                                                                                                                                                                                                                                                                                                                                            tctgccagttctatgtggtgaacagtgagtgtcctgccagctgtaccagagatcgggag 757
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TITLE OF INVENTION: WETHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
                                                                                                                                                                                   Score 121.2; DB 3;
Pred. No. 1.7e-22;
6; Mismatches 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 3479 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                       7.9%;
                                                                                                                                                                                         Query Match 7.9 Best Local Similarity 56.8 Matches 268; Conservative
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APPLICANT: Benton, Bret
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STATE: California
COUNTRY: U.S.A.
                                                                                                              ; TOPOLOGY: linear
US-08-714-918-7
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US-09-265-315-7/C
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goagaatacagagatatggaatcagattattcaggacagggagttgaccaactgcaaaga 594
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NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
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ZIP: 10036
COMPUTER READABLE FORM:
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STREET: 1185 AV
CITY: New York
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US-08-757-669A-17/C
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                                   APPLICANT: Bohenzky, Roy A.

APPLICANT: Russo, James J.

APPLICANT: Russo, James J.

APPLICANT: Modelman, Isidore S.

APPLICANT: Modelman, Isidore S.

TITLE OF INVENTION: POLYPEPFIDES FROW KAPOSI'S SARCOMA-ASSOCIATED

TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF

CORRESPONDENCES 20

CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 387.4; DB 2;
Pred. No. 1.1e-92;
0; Mismatches 341;
                                                                                                                                                                                                    3: Cooper & Dunham LLP
1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/770,37
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 5234:
TELECOMOUNICATION INFORMATION:
TELECHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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Best Local Similarity 63.5
Matches 592; Conservative
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                     APPLICANT: Chang, Yuan
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                   New York
                                                                                                                                                                                                                                                                                      U.S.A.
GENERAL INFORMATION:
                                                                                                                                                                                                                                                New York
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                                                                                                                                                                                                                                                                                    COUNTRY: U ZIP: 10036
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20603 GCGCCCTACGTGGACGCGGATGCTGTATACAGGCCAGGGGTTTGACCAATTGTCGTAC 2054
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                                                      gigatigacaccatcaaaaccaacctgacgacagaagaatcatcatgigcgctiggaat 654
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APPLICANT: Russo, James J.
APPLICANT: Rallman, Isidore S.
APPLICANT: Moore, Patrick S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS TITLE OF INVENTION: SOUTH AND USES THEREOF NUMBER OF SEQUENCES. 20
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APPLICATION NUMBER: US/08/757,669A
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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15570 gtcgtacaattatggcaaaataatggccttattttgtttttagcttcagcgagaacccag 1562
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; Patent No. 6210950
; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.8%;
Matches 1533; Conservative
; PAGES: 2035-2043
; DATE: 25-MAR-1985
US-09-089-195-1
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LORYIDTIKTNDDDRRIINCANNPRDLPIMALPPCHALCOFYVNSELSCQLYQRSG
MGLGVPFNIASYALLTYMIAHITGLKPGDFIHTLGDAHIYLNHIEPLKIQLQFREPRP
                                                                                                                                                                                                                                                                                              /translation="MPVAGSELPRRPLPPAAQERDAEPRPPHGELQYLGQIQHILRC
VRKDDRTGTGTLSVFGMQARYSLRDEFPLLTTKRVFWKGVLBELLWFIKGSTNAKEL
                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:22884 IMAGE:4048625"
/tissue_type="Bone marrow, chronic myelogenous leukemia"
/lab_host="MHH MGC_54"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1533)
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Submitted (05-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1029 gcagatecaacaeatectecgetgeggegteaggaaggaegaeegeaegggeaeeggeae 1088
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                                                                                                                                                                                                                                 /product="Similar to thymidylate synthetase"
/protein_id="AAH13919.1"
/db_xref="GI:15530267"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 277; DB 9; Length 1569;
Pred. No. 1.6e-38;
0; Mismatches 5; Indels
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NIH-MGC Project URL: http://mgc.nci.nih.gov
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                                                                                                                                                               /note="Vector: pDNR-LIB" 96. .1037
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Email: cgapbs-r@mail.nih.gov
  Location/Qualifiers
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98.2%;
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ORIGIN
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KEYWORDS
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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
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Homo sapiens, Similar to thymidylate synthetase, clone MGC:22884
IMAGE:4048625, mRNA, complete cds.
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Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Ketteman and Anuradha Madan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1569)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           961 Ctgoccccgccgcacaggagoggagogcgacgcgccgccgcagagggagctgcag 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TIGCCCCCCCCCCACACACACGCGGACCCGACCCGCGTCCGCCGCCACGGGGGAGCTGCAG 180
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                                                                                                                                                                                                                                            Length 3298;
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                                                                                                                                                                                                                                              Score 287.2; DB 6;
Pred. No. 2.7e-40;
                                                                                                                                                                                                                                                                                            4;
                                                                                                                                   /note="Incyte ID No: 247220.15"
709 c 744 g 919 t
    WO 0177389-A 200 18-OCT-2001;
                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Patent: WO 017/305 a. ____
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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98.6%;
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Best Local Similarity
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KEYWORDS
           JOURNAL
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OY 902 etcegtccccegccegcceatgcctgtggccggctcggagctgccggcccC 961	Oy 962 tgcccccgccgcacaggagcgggacgcgcgcgcgcgccgcacggggagctgcagt 1021 	Oy 1022 acctggggcagatccaacacatcctccgctgcggcgtcaggaagga	1082	1142	SULT 10 3.88476	LOCUS AX348476 1186 bp DNA linear PAT U6-FEB-2U02 DEFINITION Sequence 171 from Patent W00202806. ACCESSION AX348476. VVERTON AX348476.1 GI:18614512	synthetic cc ISM synthetic cc	REFERENCE 1 (sites) ATTHE AUTHORS OLEK,A., Piepenbrock,C. and Berlin,K. TITLE Method and nucleic acids for pharmacogenomic methylation analysis JOHNNAL PATENT: WO 0202806-A 171 10-03M-2002;	Epigenomi ce	/db_xref="taxon:32630" /note="chemically treated genomic DNA (Homo sapiens)" BASE COUNT 224 a 98 c 347 g 517 t ORIGIN	atch 59.7%; Score 708.4; DB 6; Length 1186; cal Similarity 75.1%; Pred. No. 8.8e-113;	Matches 891; Conservative 0; Mismatches 295; Indels 1; Ga 1 gatcgccactgcactccagcctgggtgagagaggggagactctgtctcaaaaaaaa	Db 1 GATCGCGTTATTGTTTTAGTTTGGGTGAGAGCGAGATTTGTTTTAAAAAAAA	OY 121 tittittittittittitggacagtottgctctgtcgcccaggctggagtacaatggt 180	OY 181 oggatottggotcactgcaactttgcotcccaggttcaagcaattcttctgcctcagcc 240	Oy 241 toccaagtagccaccacgctaatttttgtanttttagtagagagggtttcac 300	Oy 301 catgitgtccaggctggtctngaactcctgacctcaggtgatccacccgcctcggcccc 360

Unpublished

TITLE JOURNAL

AUTHORS

human.

ORGANISM

REFERENCE AUTHORS

DEFINITION AC020697/c

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ACCESSION

KEYWORDS VERSION

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19650 Crossaaagcccrsscscr---rrrrrrrrrrrrrrrrrrrrrrrrrggaaaagccacacrcrr 19594
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                                        1440 9151: contig of 7712 bp in length 9152 9251: gap of 100 bp 9252 19650: contig of 10399 bp in length 19651 19750: gap of 100 bp 19751 34038: contig of 14288 bp in length 10751 34039 47818: gap of 100 bp 100 b
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/clone_lib="RPCI-11 Human Male BAC"
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0; Mismatches 11;
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/note="assembly_fragment"
47418 a 35541 c 35457 g 46526 t
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96.2%; Pred. No. 1.4e
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/note="assembly_fragment"
89132. .116606
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9151: contig of 7
51: gap of 100
19650: contig of 1
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Matches 1055; Conservative
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Unpub
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                                                                                                                                                                                 ACO20697

Homo sapiens chromosome 18 clone RP11-145B19 map 18, WORKING DRAFT SEQUENCE, 9 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165742)
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center clone name: 145_B_19
Center clone name: 145_B_19
Sequencing vector: M13, M77815; 100% of reads
Sequencing vector: M13, M77815; 100% of reads
Assembly program: Phrap, version 0.960731
Consensus quality: 160695 bases at least Q40
Consensus quality: 161157 bases at least Q30
Consensus quality: 164107 bases at least Q30
Insert size: 164000; agarose-fp
Insert size: 164000; agarose-fp
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
1217 GGCCCCTGCGGGACGGGTGGCGGGAAGGAGGGAGGCGCGCGGGGA 1263
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TITLE

COMMENT

	1021	1157	OY 1141 GGCCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGG		DEFINITION HOMO Sapid ACCESSION D00596 VERSION D00596.1	ACIWOKUS LUMMISAJIA SOUNCE HOMO SADI ORGANISM HOMO SADI	RS	TITLE STRUCTURA SOUTHASE JOURNAL J. BIO1. MEDLINE 91056070	COMMENT These date Kaneda National 1111 Yata		FEATURES	repeat_unit	repeat_unit	prim_transcript (prim_transcript (prim_t	prim_transcript { repeat_unit {	repeat_unit 6	SOD	
	1;																	
NT 4521 a 3991 c 4479 g 5605 t	<pre>// Match Local Similarity 99.0%; Score 1163.8; DB 6; Length 18596; Local Similarity 99.1%; Pred. No. 3e-191; les 1176; Conservative 0; Mismatches 10; Indels 1; Gaps</pre>	1 gatogogocactgoactcoagoctgggtgagagagogagactctgtctcoaaaaaaaa 60	l aaaaagacogccagggttcaaacaaaaacttoggaaaagcoctggcggtcttttttt 120 	1 ttttttttttttttttttgggacagtcttgctctgtcgcccaggctggagtacaatggt 180	oggatottggotoactgoaacototgcotocoaggttoaagoaattottotgcotoagoc 240	1 tcccaagtagccaccacgccagctaatttttgtanttttagtagagaggggtttcac 300	l catqttgtccaggctgqtctngaactcctgacctcaggtgatccacccggctcggcccc 360	l caaagtactaggattacaggcgtgagccaccgcgtccagcgccctggcggtttttaatca 420 	agtagaaagctgcattataccacttgcttcngttgcnttcagtgagaacgaagaaatgg 480	l aaatgcaaatAncttattagttgtaggaaacagatctcaaacagcagtttgtngacaag 540 	1 accgcaggaaacgtgggaactgtgctgtgttagagaaggcgcggtcgaccagacgg 600 	1 tteccaaaggegeagteettecengecaectgentecaggttecegggnteet 660	agactotcagotgtggccotgggotcogttotgtgccacacocgtggctcotgcgtttc 720		1. gagogogggacggcgcggggaaaaggcgcgcggaagggtcctgccaccgcgccacttgg 840 	cctgcctccgtcccgccgcgcacttggcctccgtcccgccgccgccacttcgcctg 900	L ectecytececogecogecogagecatgectgtggceggeteggagetgeegegeegee 960	
BASE COUNT ORIGIN	Query Match Best Local : Matches 117	Qy dd	Qy 61 Db 138	Qy 121 Db 198	Qy 181 Db 258	Oy · 241 Db 318	Qy 301 Db 378	Qy 361 Db 438	Oy 421 Db 498	Qy 481 Db 557	Qy 541 Db 617	Qy 601 Db 677	Qy 661 Db 737	Qy 721 Db 797	Qy 781 Db 857	Oy 841 Db 917	Qy 901 Db 977	Qy 961

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18596 bp DNA linear PRI 14-APR-201 eles gene for thymidylate synthase, exons 1, 2, 3, 4, 5, 1 ete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ta kindly submitted in computer readable form by: Sumiko
                                                      join(1001. .1205,2895. .2968,5396. .5570,11843. .11944,
11449. .13624,14133. .14204,15613. .15750)
/EC_number="2.1.1.45"
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., Nalbantoglu, J., Takeishi, K., Shimizu, K., Gotoh, O.,
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pt 822. .477
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iens DNA, clone:lambdaHTS-1 and lambdaHTS-3.
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Chem. 265 (33), 20277-20284 (1990)
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/note="inverted repeat"
904. .993
/note="triple tandem repeats"
<1001. .1205
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1. .18596
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+81-559-71-3651
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Sat Jul

Query Match Best Local Sin	Marches 11/5; Qy 1 gatego	Db 78 GATCGC	Db 138 AAAAG Qy 121 ttttt	Db 198 TITITI Qy 181 cggatc	Db 258 CGGATC Qy 241 tcccaa		Db 378 CATGIT QY 361 caaagt	 Db 438 CAAAGT Qy 421 agtaga	 Db 498 AGTAGA Qy 481 aaatgo	Db 557 AAATGC QY 541 accgca	Db 617 ACGCA Qy 601 ttccca	Db 677 TTCCCCC Qy 661 aagact Db 737 AAGACT Qy 721 cccctg	797	 Db 857 GAGGGC Qy 841 cctgcc	 Db 917 ccrgcc	OY 901 cctccg Db 977 CCTCCG	Qy 961 Ctgccc Db 1037 TTGCC
		Oy 601 ttcccaaagggcgcagtccttcccngccaccgcactgcntccagttcccgggtntcct 660	Oy 661 aagactctcagctgtggccctgggctccgttctgtgccacaccggtggctcctgggttc 720	OY 721 ccctggcgcacgctctctagagcggggccgccgcgccgc	OY 781 gagcgcgggacggcggggaaaaggcgcgcgggaaggggtcctgccaccggccacttgg 840	QY 841 octgectcogtcogcogcacttggcctgcctccgcogcogcacttggctg 900	OY 901 cetecgteceegeegegeeatgeetgtggeeggeteggagetgeegggee 960	QY 961 Ctgcccccgccgcacaggagcgggacgccgagccggcgcacagggggg	OY 1021 tacttggggcagatccacacatctccgctgcggcgtcaggaagga	QY 1081 accggcaccctgtcggtattcggcatgcaggcgcgctacagcctgagaggtgacgccggg 1140	OY 1141 ggccctgcgggacgggtggggaaggaggcggcggctgggga 1187 	RESULT 4 AX330682 LOCUS LOCUS AX330682 LOCUS DEFINITION Sequence 1191 from Patent W00194629. VERSION AX330682.1 GI:18103660	KEYWORDS SOURCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	CE 1 (sites) Eutheria; Frimates; Catarrhin; Hominidae; RS Young, E., Augustus, M., Carter, K.C., Ebner, R., Endr Horrigan, S., Soppet, D.R. and Weaver, Z.	Jills Canter gene determination and therapeutic screening using signature gene sets JOURNAL Patent: WO 0194629-A 1191 13-DEC-2001;	Avalon Pharmaceuticals (US) EPATURES Location/Qualifiers Source 118596 Agranism="Homo sanians"	/db_xref="taxon:9606"

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Score 1163.8; DB 6; Length
Pred. No. 3e-191;
0; Mismatches 10; Indels
 98.0%;
99.1%;
               Conservative
        milarity
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1 (bases 1 to 18596)
Johnson, W.G. and Stenroos, B.Scott.
Methods for diagnosing, preventing, and treating developmental
disorders due to a combination of genetic and environmental factor.
Patent: US 6210950-A 11 03-APR-2001;
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Sequence 11 from patent US 6210950.
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AR144965.1 GI:15106832
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AMENGABEL TO AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cartivity, and can be used in gene therapy and vaccine production. (I) creatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased cample, they may be used to treat disorders associated with decreased cample, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or to cyplement the patients own production of (I). Additionally, (I) projucteofides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the clargnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic artige genomic cancers and cancer metastases of haematopoietic artige genomic sequences from the present invention. AAK54912 to AAK54950 and AAM82169 very represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 34572; 3071pp + Sequence Listing; English.
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                                                                110 tettittittittittittittittittitgggacagtettgetetgtegecaggetgg 169
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Matches 270; Conservative
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Query Match

20000S-0229509

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                            331 acctcaggtgatccacccgcctcggccccccaaagtactaggattacaggcgtgagccac 390
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                                                                        4499 TGTGCCCGGCGCTCTGTAGCATTTTCACTTAATAAA 4464
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Ruben SM;

Rosen CA, Barash SC, WPI; 2001-483426/52

(HUMA-) HUMAN GENOME SCI INC

20000S-0251479. 20000S-0251856. 20000S-0251868.

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) activity, and can be used in gene therapy and vaccine production. (I) proteins and polyuncleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to pulpulement the patients own production of (I). Additionally, (I) polyuncleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, and cancer matationally cancer matationally dispasses, especially cancers and creat immune/haematopoietic-related dispasses, especially anc cancers and cancer metastases of hematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention. 1834 gattgtgccactgcactccagcctgggtgacagagcaagactctatctcaaaaaactaaa 1893 1894 taaataatgaaaaactcagtgcagatactgggcatctaggtttttct----tttctttc 1949 2010 gigatotoggotoactgcagcototogoctoctaggitoaagcgattotoctgcotoagco 2069 aaaaagaccgccagggctcaaacaaaaacctcggaaaagccctggcggtctttttt 120 tttttttttttttttttgggacagtcttgctctgtcgcccaggctggagtacaatggt 180 oggatettggctcactgcaacctctgcctccaggttcaagcaattcttctgcctcagcc 240 281 Score 204.2; DB 22; Length 56743; Pred. No. 1.2e-26; 0; Mismatches 105; Indels 24; Gaps 2070 toccgagtagctggaattacaggcgcccaccatgcccggctaattttgtattttta Disclosure; SEQ ID NO 36572; 3071pp + Sequence Listing; English. Sequence 56743 BP; 14298 A; 13270 C; 14240 G; 14935 T; 0 other; Query Match 17.2%; Best Local Similarity 71.3%; Matches 320; Conservative (tcccaagtag-----1950 121 61 181 241 ğ 쉽 δ 셤 δŽ 음 qq δ $Q\overline{Q}$ QQ δŽ

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08-SEP-2000;
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     09-AUG-2001
     32
activity, and can be used in gene therapy and vaccine production. (I)

proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased

expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
coplanciectides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynuclectides may be used to prevent.
If agnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic derived cells. AAK64703

to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK64921 to AAK64950 and AAM881169
                                                                                                                                                                   represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 gtcggatcttggctcactgcaacctctgcctcccaggttcaagcaattcttctgcctcag 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 gatecaccegecteggecececeaaagtactaggattacaggegtgagecaccgegtecag 399
                                                                                                                                                                                                                                                                                                                        61 aaaaagaccgccagggctcaaacaaa-aaacctcggaaaagccctggcggtctttttt 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                          1 gatogogocactgoactcoagoctgggtgagagagogagactctgtctoaaaaaaaaa 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21686
                                                                                                                                                                                                                             17.2%; Score 204.6; DB 22; Length 11553; 72.0%; Pred. No. 9.8e-27; tive 0; Mismatches 101; Indels 22; C
                                                                                                                                                                                           Sequence 11553 BP; 3513 A; 2418 C; 2597 G; 3025 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK66874 standard; DNA; 37449 BP.
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Matches 316; Conservative
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AC AAK666
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KW Human,
KW Cytost
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in per therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and expression by reactifying mutations or delections in a perient's generalized expression by rectifying mutations or delections in a perient's genome supplement the patients of (I) by expressing inactive proteins or to the nucleic decides may be used to product on of (I). Additionally, (I) the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding human immune/hematopoietic antigen polypeptides, metastasis .
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                                                                                                   08 NOV-2000; 2000US-0246532

08 NOV-2000; 2000US-0246609

08 NOV-2000; 2000US-0246611

08 NOV-2000; 2000US-0246611

17 NOV-2000; 2000US-0246613

17 NOV-2000; 2000US-0249207

17 NOV-2000; 2000US-0249209

17 NOV-2000; 2000US-0249210

17 NOV-2000; 2000US-0249211

17 NOV-2000; 2000US-0249211
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17-NOV-2000; 2000US-0249216.
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249244.
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2000US-0246609.
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17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297
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2000US-0251868
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05-JAN-2001; 2001US-0259678.
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08-NOV-2000; 2
08-NOV-2000; 2
                        08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
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08-DEC-2000;
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7743 GTGCGATCTCAGCTCAACCTCTGCCTCCTGGATTCAAGTGATTCTCCTGCCTCAG 7684
                                                                                                                    61 aaaaagaccgccagggctcaaacaaa--aaacctcggaaaagccctggcggtctttttt 118
                                                                                                                                                             119 ttttttttttttttttttgggacagtcttgctctgcccaggctggagtacaatg 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28083.
                                                                                                                                                                                                                                                  239 octoccaagtag------ccaccaccaccagccaattttgtanttt
                                   17.2%; Score 204.6; DB 22; Length 11453; 72.0%; Pred. No. 9.8e-27; tive 0; Mismatches 101; Indels 22; (
Sequence 11453 BP; 3521 A; 2392 C; 2561 G; 2979 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic, gene therapy; vaccine; metastasis; ds.
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                               Query Match 17.2'
Best Local Similarity 72.0'
Matches 316; Conservative
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24-FEB-2000; 2000US-0184664
02-MAR-2000; 2000US-0186350,
16-MAR-2000; 2000US-0186350,
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Obnoers and cancer metastases of haematopoietic-derived cells. AAK677 sequences from the present human immune/haematopoietic antigen genomic represent sequences used in the exemplification of the present invention.

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gagtgcaatggcacgatctcggctcactgcaacatctgcctcccaggttcaagcaattct 5478
                                                                                                                             gacctcaggtgatctgcctgcctcggcctcccaaagtcctgggattacaggcatgagcca 5657
                                                                                                                                                                     5658 ccacgcccagctactttacctttcatatttgtcattattttgtggataataatgaagaat 5717
                                                                                                                                                                                                      Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                          450 tongttgentteagtgagaacgaagaaatggaaatggaaatgcaaatAnettattagttgtaggaa
                                           cctgcctcagcctcccaagtagctaggactacaggcacctgccaccaccagctaatt
                                                               tttgtanttttagtagagacgggggtttcaccatgttgtccaggctggtctngaactcct
                                                                                                         gacctcaggtgatccacccgcctcggcccccaaagtactaggattacaggcgtgagcca
                                                                                                                                                 cogcottccagcocctggcggtttttaatcaagtagaaaagctgcattataccacttgct
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                     tetgeeteageeteceaagta----
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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                                                                        2000US-0246610
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08-NOV-2000;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or
New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Gaps

20;

Indels

Score 206.4; DB 22; Pred. No. 4.8e-27; 0; Mismatches 111;

17.48; 70.38;

Best_Local Similarity 70.3 Matches 310; Conservative

Query Match

DB 22; Length 9731;

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109 gtottttttttttttttttttttttttttttgggacagtcttgctctgtcgcccaggctg 168

169 gagtacaatggtcggatcttggctcactgcaacctctgcctcccaggttcaagcaattct 228

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2000US-0226279
                                       1000US-0226681
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02-0CT-2000;
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2000US-0246613 2000US-0249207 2000US-0246510 2000US-0246611 2000US-0249208 2000US-0246609 2000US-0249214 08-NOY-2000; 08-NOY-2000; 08-NOY-2000; 08-NOY-2000; 08-NOY-2000; 08-NOY-2000; 08-NOY-2000; 17-NOY-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 05-DEC-2000; 05-DEC-2000; 06-DEC-2000; 08-DEC-2000; 08-DEC-2000; 08-DEC-2000; 17-NOV-2000; 7-NOV-2000; 17-NOV-2000; 01-DEC-2000; 01-DEC-2000; 05-DEC-2000; 05-JAN-2001;

(HUMA-) HUMAN GENOME SCI INC

Ruben SM, Rosen CA, Barash SC,

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 20393; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
concers and cancer metastases of haematopoietic artigen genomic
concers and acrose metastases of haematopoietic artigen genomic
sequences from the present invention. AAK54912 to AAK84950 and AAM82169
crepresent sequences used in the exemplification of the present invention.

Sequence 56632 BP; 17016 A; 8910 C; 10552 G; 20154 T; 0 other;

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2000US-0226279.
2000US-0226681.
2000US-0226868.
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 Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antidifammatory; antidicer; vulnerary; anticonvulsant; antidacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein;
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an analyte in a analyte-binding
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                                                      The present invention relates to a method for assaying an analyte is sample comprising; contacting the sample with a mutant analyte-bind enzyme which has binding affinity for the analyte or an immediate analyte enzymeatic conversion product but has attenuated catalytic activity; and detecting resulting binding. The method is useful in monitoring biological systems/processes, or prognosis/diagnosis of disease caused by imbalances of the analytes. The present sequence a coding sequence used in the present invention.

Note: the present sequence is not shown in the specification, but we
                                                                                                                                                                                                                                                                the specification.
                                                                                                                                                                                                                                                                                                           Sequence 18596 BP; 4521 A; 3991 C; 4479 G; 5605 T; 0 other;
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                      English,
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                    Disclosure;
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 Length 18596;
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 22;
Score 1163.8; DB 22
Pred. No. 8.6e-192;
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98.0%;
ilarity 99.1%;
Conservative
           Similarity
          Best Local Sim
Matches 1176;
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The present invention provides a novel method of estimating the susceptibility of an individual to a developmental disorder using genetic and environmental variables. The method can be used in the diagnosis, prevention and treatment of disorders such as schizophrenia, spina bifida cystica, Tourette's syndrome, bipolar illness, autism, conduct disorders, attention deficit disorder, obsessive compulsive disorder, chronic

Disclosure; Page 125-131; 156pp; English.

DS with reference DS

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Tourette's syndrome; bipolar illness; autism; conduct disorder;
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                                            cotgootcogtocogocgocacttggcotgcotcogtcocgcogcgccacttcgcctg
           gagegeggaeggeeggggaaaaggegegegeggaaggggteetgeeaeegegeeaettgg
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attention deficit disorder; obsessive compulsive disorder;
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/lab_host="DH10B (phage-resistant)"
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Directionally cloned into ECORIXAhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1:8Bb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                           EST 21-MAR-2001
                                                                                                                                                                                                                                                      E 1 (bases 1 to 524)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Topublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: ogapbs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Consortium/Link at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

High quality sequence stop: 524.

Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                   BG482405
602526568F1 NIH_MGC_21 Homo sapiens CDNA clone IMAGE:4650280 5',
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96.0%;
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Matches 309; Conservative
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AUTHORS
            RESULT 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pCMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 935)
11, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Matches 280; Conservative
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/note="Wector: pME185FL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"
216 c 212 g 143 t 3 others
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Memora I to 738)
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; CDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
              acgggggagctgcagtacctgggggcagatccaacacatcctccgctgcggcgtcaggaagg 1066
                                                                                                                                                                       Ota'I., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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Pred. No. 2.5e-26;
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
18-181-1848-52-3951
Pax: 81-438-52-3952
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/db_xref="taxon:9606"
/clone="NUZPR9100412"
/clone_lib="NUZRP3"
/cell_type="teratocarcinoma"
/cell_line="NT2"
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Contact: Takao Isogai
Genomics Laboratory
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http://fullianguistech.com URL:
http://fullianguistech.com uRL:
1 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                               880 cccgccgccacttcgcctgcctccgtcccccgccgccgcgcgcatgcctgtggccggc 939
                                  940 toggagotgoogooggoooOtgooocogoogoaaaggagogggacgoogagoogt 999
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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/clone="CSODIO60YE04"
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/tissue_type="placenta"
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